

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:23:17 ; Search time 26.6667 Seconds  
(without alignments)  
744.081 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAQVLMILLWVSGTCG.....EVTHQGLSPVTKSFNRGEC 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	93.8	240	US-09-301-593-28	Sequence 28, Appl
2	1136	91.4	240	US-09-301-593-36	Sequence 36, Appl
3	1122	90.3	240	US-10-630-406-8	Sequence 8, Appl
4	1121.5	90.2	239	US-09-627-896B-22	Sequence 22, Appl
5	1120.5	90.1	241	US-07-916-098A-56	Sequence 56, Appl
6	1070	86.1	220	US-09-301-593-17	Sequence 17, Appl
7	1064	85.6	220	US-08-952-235-1	Sequence 1, Appl
8	1064	85.6	220	US-09-669-971-1	Sequence 1, Appl
9	1019.5	82.0	239	US-08-812-586-29	Sequence 29, Appl
10	1019.5	82.0	239	US-09-535-832A-30	Sequence 30, Appl
11	994.5	80.0	235	US-09-472-087-14	Sequence 14, Appl
12	994.5	80.0	235	US-09-472-087-65	Sequence 65, Appl
13	991.5	79.8	233	US-09-472-087-15	Sequence 15, Appl
14	991.5	79.8	233	US-09-472-087-67	Sequence 67, Appl
15	987	79.4	236	US-09-859-053-34	Sequence 34, Appl
16	985	79.2	234	US-09-472-087-17	Sequence 17, Appl
17	985	79.2	234	US-09-472-087-69	Sequence 69, Appl
18	977	78.6	236	US-09-859-053-38	Sequence 38, Appl
19	974.5	78.4	239	US-10-000-489-8	Sequence 8, Appl
20	973	78.3	234	US-09-848-832-4	Sequence 4, Appl
21	969	78.0	234	US-09-049-672A-6	Sequence 6, Appl
22	967	77.8	236	US-09-859-053-30	Sequence 30, Appl
23	955.5	76.9	239	US-08-487-550-6	Sequence 6, Appl
24	955.5	76.9	239	US-09-526-098-6	Sequence 6, Appl
25	955.5	76.9	239	US-09-383-916-6	Sequence 6, Appl
26	955.5	76.9	239	US-09-758-173-6	Sequence 6, Appl
27	955.5	76.9	239	US-09-576-424-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-301-593-28  
; Sequence 28, Application US/09301593A  
; Patent No. 6455677

GENERAL INFORMATION:

; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leiger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652 1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-301-593-28

Query Match 93.8%; Score 1166; DB 2; Length 240;

Best Local Similarity 93.3%; Pred. No. 2.9e-88;

Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY	1	MDSQAQVLMILLWVSGTCGDIWVSQSPSLAVSLGERTVLTNCKSSQSLLYSQNKNYLA	60
DB	1	MDSQAQVLMILLWVSGTCGDIWVSQSPSLAVSLGERTVLTNCKSSQSLLYSQNKNYLA	60
QY	61	WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEDVAVYCCQYYSY	120
DB	61	WYQQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEDVAVYCCQYYSY	120
QY	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL	180
DB	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL	180
QY	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	240
DB	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	240

RESULT 2

US-09-301-593-36

```
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match      91.4%; Score 1136; DB 2; Length 240;
Best Local Similarity 90.0%; Pred. No. 8.4e-86;
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA 60
DB 1 METDTLLWVLLWVPGSGDVTMTQSPDSLAVSLGERATINCKSSQSLLYSRNOKNYLA 60

QY 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSY 120
DB 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSY 120

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
DB 121 PLTFGAGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 3
US-10-630-406-8
; Sequence 8, Application US/10630406
; Patent No. 6887673
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic

US-09-627-896B-22
; Sequence 22, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: 3D1 light chain
US-09-627-896B-22

Query Match      90.2%; Score 1121.5; DB 2; Length 239;
Best Local Similarity 90.4%; Pred. No. 1.3e-84;
Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLA 60
DB 1 MDSQAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLSRTRENYLA 60

QY 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSY 120
DB 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSY 120

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
DB 121 -YTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 179

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 180 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239
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RESULT 5  
US-07-916-098A-56  
; Sequence 56, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.  
; APPLICANT: CHISHOLM, PATRICIA L.  
; APPLICANT: THOMAS, DAVID W.  
; APPLICANT: ROSA, MARGARET D.  
; APPLICANT: ROSA, JOSEPH J.  
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
; STREET: 10 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/916,098A  
; FILING DATE: July 24, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/08843  
; FILING DATE: No. 5871732ember 27, 1991  
; CLASSIFICATION: 424  
; APPLICATION NUMBER: 07/618,542  
; FILING DATE: No. 5871732ember 27, 1990  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JOHN J. MC DONNELL  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,310-G  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; TELEX: 910/221-5317  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-916-098A-56

Query Match 90.1%; Score 1120.5; DB 1; Length 241;  
Best Local Similarity 92.4%; Pred. No. 1.6e-84;  
Matches 218; Conservative 6; Mismatches 11; Indels 1; Gaps 1;  
QY 5 AQLMLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQQ 64  
DB 7 AQLGLLLWLPARGDIVMTQSPDSLAVSLGERATINCKSSGSLLYSTNQKNYLAWYQQ 66  
QY 65 KFGQSPKLLIYWASARESGVPRFSGSGGTDFTLTISSVQAEADVAVVYCCQYYSYPLTF 124  
DB 67 KFGQPPKLLIYWASTRESGVPRFSGSGGTDFTLTISSLQAEADVAVVYCCQYYSY-RTF 125  
QY 125 GAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGN 184  
DB 126 GRGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGN 185  
QY 185 SQESVTEQDSKSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 186 SQESVTEQDSKSTYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 6  
US-09-301-593-17  
; Sequence 17, Application US/09301593A  
; Patent No. 6455677  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-17  
Query Match 86.1%; Score 1070; DB 2; Length 220;  
Best Local Similarity 93.2%; Pred. No. 2e-80;  
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQQKPGQSPKLLIYWASAR 80  
DB 1 DIVMSQSPDSLAVSVGEKVTMSCKSSQSLLYSRNKNYLAWFQOKPGQSPKLLIFWASTR 60  
QY 81 ESGVPRFSGSGGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140  
DB 61 ESGVPRFSGSGGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRITVAAPS 120  
QY 141 VFIPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200  
DB 121 VFIPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180  
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 7  
US-08-952-235-1  
; Sequence 1, Application US/08952235  
; Patent No. 6207152  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; APPLICANT: Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; TITLE OF INVENTION: Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/952,235  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-08-952-235-1  
  
Query Match 85.6%; Score 1064; DB 2; Length 220;  
Best Local Similarity 90.9%; Pred. No. 6.2e-80;  
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;  
  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DIMMSQSPSSLTVSVGEKVTVCCKSSQSLTYTSSQKNVLAWYQKPGQSPKLLIYWASTR 60  
  
QY 81 ESGVPRDFRSGSGGDTFTLTITSSVOAEDVAVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140  
Db 61 ESGVPRDFRSGSGGDTFTLTITSSVKADDLAVYCCQYIAYPWTFGGTTKLEIKRTVAAPS 120  
  
QY 141 VFIFPPDSQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDYTS 200  
Db 121 VFIFPPDSQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDYTS 180  
  
QY 201 LSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 240  
Db 181 LSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 220  
  
RESULT 8  
US-09-669-971-1  
; Sequence 1, Application US/09669971  
; Patent No. 6468529  
; GENERAL INFORMATION:  
; APPLICANT: Schwall, Ralph H.  
; Tabor, Kelly H.  
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
; Antagonists and Uses Thereof  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/669,971  
; FILING DATE: 05-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/952,235  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/460368  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P0938P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-669-971-1  
  
Query Match 85.6%; Score 1064; DB 2; Length 220;  
Best Local Similarity 90.9%; Pred. No. 6.2e-80;  
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;  
  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DIMMSQSPSSLTVSVGEKVTVCCKSSQSLTYTSSQKNVLAWYQKPGQSPKLLIYWASTR 60  
  
QY 81 ESGVPRDFRSGSGGDTFTLTITSSVOAEDVAVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140  
Db 61 ESGVPRDFRSGSGGDTFTLTITSSVKADDLAVYCCQYIAYPWTFGGTTKLEIKRTVAAPS 120  
  
QY 141 VFIFPPDSQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDYTS 200  
Db 121 VFIFPPDSQLSGTASVCLLNFPYKAVQKVDNALQSGNSQESVTEQDSKDYTS 180  
  
QY 201 LSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 240  
Db 181 LSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 220  
  
RESULT 9  
US-08-812-586-29  
; Sequence 29, Application US/08812586  
; Patent No. 6048704  
; GENERAL INFORMATION:  
; APPLICANT: Martin David Tilson  
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
; PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/812,586  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/53862-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-29

Query Match      82.0%; Score 1019.5; DB 2; Length 239;
Best Local Similarity 85.2%; Pred. No. 3.1e-76;
Matches 201; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 4 QAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLAWYQ 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 QTQVFISLLLLWISG-AGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVVYCOQYYSPLT 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 QKPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDFVAVYQGYGSSPLT 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 183
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FGGGTKEIKRTVAAPSVFIFPPSDEQLKEITASVVGLLNNFYPREAKVQWKVDNALQSG 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 183 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-09-535-832A-30
; Sequence 30, Application US/09535832A
; Patent No. 653769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: With Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-30

Query Match      82.0%; Score 1019.5; DB 2; Length 239;
Best Local Similarity 85.2%; Pred. No. 3.1e-76;
Matches 201; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 4 QAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLAWYQ 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 QTQVFISLLLLWISG-AGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVVYCOQYYSPLT 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 QKPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDFVAVYQGYGSSPLT 122
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSG 183
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 FGGGTKEIKRTVAAPSVFIFPPSDEQLKEITASVVGLLNNFYPREAKVQWKVDNALQSG 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 184 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 183 NSQESVTEQDSKDSYSLSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      80.0%; Score 994.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.5e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;

QY 1 MDSQAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 METPAQLLFLLLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 WYQOKPGQSPKLLIYWASARESGVDPDRFSGSGSGDTFTLTISVQAEADVAVVYCOQYYS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 56 WYQORPGQAPRLLIYDASSRATGIPDRFSGSGSGDTFTLTISRLEPEDFVAVYCOQYGS 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 116 PWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      80.0%; Score 994.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.5e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;

QY 1 MDSQAQVLMALLLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSQNKNYLA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 METPAQLLFLLLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTITSRLEPEDFAVYCOQYGTGS 115
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 116 PWTFGGKTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 175
QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235
```

```
RESULT 13
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15
```

```
Query Match 79.8%; Score 991.5; DB 2; Length 233;
Best Local Similarity 79.2%; Pred. No. 6e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRTSVS-----SSYLA 53

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 54 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTITSRLEPEDFAVYCOQYGTGS 113

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 114 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 173

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 233
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```
RESULT 14
US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
```

```
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-67
```

```
Query Match 79.8%; Score 991.5; DB 2; Length 233;
Best Local Similarity 79.2%; Pred. No. 6e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRTSVS-----SSYLA 53

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 54 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTITSRLEPEDFAVYCOQYGTGS 113

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 114 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 173

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 233
```

```
RESULT 15
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34
```

```
Query Match 79.4%; Score 987; DB 2; Length 236;
Best Local Similarity 78.8%; Pred. No. 1.4e-73;
Matches 190; Conservative 27; Mismatches 18; Indels 6; Gaps 2;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRAQNI-----RSSYLA 55

QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCOQYYSY 120
Db 56 WYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTITSRLEPEDFAVYCOQYGTGS 115
```







```
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 77.68; Score 965; DB 2; Length 236;
Best Local Similarity 79.7%; Pred. No. 1.3e-73;
Matches 188; Conservative 18; Mismatches 24; Indels 6; Gaps 1;

QY 5 AQVIMLLLVSGTCGDIVMSQSPDSILAVSLGSRVTLNCKSSQSLLYSGNQKNYLAQQ 64
DB 7 AQLLGLLLLVIPGARCAIQMTQSPSSLSASVGDRTVITCRASQGI-----SNDLGWYQQ 60

QY 65 KPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTITSSVQAEADVAVVYCOQYYSYPLTF 124
DB 61 KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCLQDYNYPWTF 120

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 121 GQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

QY 185 SQSVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 SQSVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 14
Q723Y4 HUMAN
ID Q723Y4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE
RP TISSUE=Skeletal Muscle;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE
RP TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
```

```
DR EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7BFEE4ED23084BC6 CRC64;

Query Match 77.5%; Score 963; DB 2; Length 236;
Best Local Similarity 79.7%; Pred. No. 1.9e-73;
Matches 188; Conservative 18; Mismatches 24; Indels 6; Gaps 1;

QY 5 AQVIMLLLVSGTCGDIVMSQSPDSILAVSLGSRVTLNCKSSQSLLYSGNQKNYLAQQ 64
DB 7 AQLLGLLLLVIPGARCAIQMTQSPSSLSASVGDRTVITCRASQDI-----SNYLAQQ 60

QY 65 KPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTITSSVQAEADVAVVYCOQYYSYPLTF 124
DB 61 KPGKAPKLLIYGASSLQSGVQSRFSGSGSGTDFTLTITSSLPQEDFATYYCOQYKSYPTF 120

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 121 GQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 180

QY 185 SQSVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 SQSVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 15
Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE
RP TISSUE=Glandular pool- thyroid;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Glandular pool- thyroid;
RC NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -, mRNA.
DR SNR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 77.2%; Score 960; DB 2; Length 236;
Best Local Similarity 78.8%; Pred. No. 3.4e-73;
Matches 186; Conservative 20; Mismatches 24; Indels 6; Gaps 1;

QY 5 AQVLM L L L L L V S G T C G D I V M S Q P D S L A V S L G E R V T L N C K S Q S L L Y S G N Q K N Y L A W Y Q Q 64
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 7 AQLGL L L L L L W F P G V R C D I Q M T Q S P S L S A S V G D R V T I T C R A S Q G I - - - - - R N D L G W Y Q Q 60

QY 65 K P Q S P K L L I Y W A S A R E S G V P D R P S G S G T D F T L T I S S V Q A E D V A Y Y C Q O Y Y S Y P L T F 124
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 61 K P G K A P K R L I F A A S S L Q S G V P S R P S G S G T E F T L T I N S L Q P E D F A T Y Y C L Y N S Y P R T F 120

QY 125 G A G T K L E L K R T V A A P S V F I P P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N 184
   ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:||||| ||:|||||
Db 121 G Q G T K V E I K R T V A A P S V F I P P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N 180

QY 185 S Q S V T E Q D S K D S T Y S L S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G E C 240
   |||||||| |||||||| |||||||| |||||||| |||||||| |||||||| |||||||| |||||||| |||||||| ||||||||
Db 181 S Q S V T E Q D S K D S T Y S L S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G E C 236
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Search completed: February 16, 2006, 10:22:55  
Job time : 126.04 secs



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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 240 AA; 26234 MW; 180D4DBB7815C4 CRC64;

Query Match      80.3%; Score 998; DB 2; Length 240;
Best Local Similarity 83.1%; Pred. No. 2.1e-76;
Matches 197; Conservative 15; Mismatches 23; Indels 2; Gaps 2;

QY 5 AQLVLLLVWVGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLAQQ 64
DB 5 AQLGLLVWVGSSGDIWVAOSPLSVTPGSPASISCRSSQSLHLS-NGNYFDWYLIQ 63

QY 65 KFGQSPKLIYWASARESVPDRFSGSGSGTDFTLTISVVQADVAIVYCCQ-YYSYPLT 123
DB 64 KFGQSPQLLIYWGSPNRPASGVDPDFSGSGSGTDFTLTKISRVEADVGVYICMQALQPPYT 123

QY 124 FGAGTKLELKRITVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 183
DB 124 FGQGTLEIKRITVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 183

QY 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGC 240
DB 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGC 240

RESULT 2
Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
AC Q52L64;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094049; AAH94049.1; -; mRNA.
DR SNR; Q52L64; 21-240.
DR InterPro; IPR003599; IG.
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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26609 MW; CF8630CCCC002B52C CRC64;

Query Match      79.3%; Score 986; DB 2; Length 240;
Best Local Similarity 76.7%; Pred. No. 2.2e-75;
Matches 184; Conservative 25; Mismatches 31; Indels 0; Gaps 0;

QY 1 MDSQAVLMLLLWVGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLA 60
DB 1 MDSQAVLMLLLWVGTCGDIWMSQSPSLAVSVGEKVTMSCKSSQSLYSYNQKNYLA 60

QY 61 WYQOKPGQSPKLIYWASARESVPDRFSGSGSGTDFTLTISVVQAEADVAVYCCQYYSY 120
DB 61 WYQKPGQSPKLIYWASTRESGVDPDFSGSGSGTDFTLTISVVKAEADLALYCCQYNY 120

QY 121 PLTFGAGTKLELKRITVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 121 PLTFGAGTKLDRRAAAPTQVIFPPSSQLTSGGASVVCFLNNFYPKQINVKWKIDGSE 180

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGC 240
DB 181 RQGVNLNSWTDQDSKDYSLSTLTLTQDEYRHNSTCEATHKTSTSPVKSFRNEC 240

RESULT 3
Q6GMV9_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
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RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073793; AAH73793.1; -; mRNA.
DR SNR; O6GNV9; 21-235
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS08335; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 79.3%; Score 985.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.3e-75;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 2;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGNQNYLA 60
Db 1 METPAQLLFLLLLWLPDITGEIVLTQSPGTLSPGERAALSCRAQSV----NSK-YLA 55

QY 61 WYQKQSQPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCCQYYS 120
Db 56 WYQKQSQPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCCQYYS 115

QY 121 PLTFAGAGTKLELXRTVAAPSFIFFPPSPDEQLKSGTASVCLLNFPYPRKAVQWKVDNAL 180
Db 116 PLTFGGGKTVKIKRTVAAPSFIFFPPSPDEQLKSGTASVCLLNFPYPRKAVQWKVDNAL 175

QY 181 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 4
Q8NEKO HUMAN
ID Q8NEKO HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (T:EMBLrel. 22, Created)
DT 01-OCT-2002 (T:EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T:EMBLrel. 26, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshnyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
RL Eur. J. Immunol. 23:3248-3262(1993).
DR EMBL; BC030814; AAH30814.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSP; P01834; 1172.
DR SMR; Q8NEKO; 21-237.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS08335; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 79.1%; Score 983.5; DB 2; Length 239;
Best Local Similarity 81.8%; Pred. No. 3.5e-75;
Matches 193; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 5 AQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGNQNYLA 64
Db 5 AQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGNQNYLA 63

QY 65 KPGQSPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCCQYYSPLTF 124
Db 64 KPGQSPKLIYASARESVPDRFSGSGGTDTFTLTISVQAEADVAVYCCQYYSPLTF 123

QY 125 GAGTKLELXRTVAAPSFIFFPPSPDEQLKSGTASVCLLNFPYPRKAVQWKVDNAL 184
Db 124 GAGTKLELXRTVAAPSFIFFPPSPDEQLKSGTASVCLLNFPYPRKAVQWKVDNAL 183

QY 185 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240
Db 184 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
Q6PIL8_HUMAN
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ID AC Q6PIL8 HUMAN PRELIMINARY; PRT; 236 AA.  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032451; AAH32451.1; -; mRNA.  
 DR HSSP; P01837; 1KCU.  
 DR SNR; Q6PIL8; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003066; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;  
 Query Match 79.1%; Score 983; DB 2; Length 236;  
 Best Local Similarity 78.4%; Pred. No. 3.8e-75;  
 Matches 189; Conservative 26; Mismatches 20; Indels 6; Gaps 2;  
 QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGRLVTLNCKSSQSLYSQGNQKNYLA 60  
 DB 1 METPAQLFLLLLWLPDSTGENVLTQSPGTLSPGERATLSRASQSL-----SSSYLA 55  
 QY 61 WYQKFGQSPKLLIYNASARESVPDRFSGSGSGTDFTLTISSVQADVAIVYCOQY-YS 119  
 DB 56 WYQKFGQAPRLIYGVSSRATGIPDRFSGSGSGTDFTLTISSRLEPDEFVAYYCOQYGS 115  
 QY 120 YPLTFAGTGLKLRVTAAPSVFIFPPSDEQLSKGTASVVCLLNNFYPREAKVQWKVDNA 179  
 DB 116 RPIIFGGTGRLDIKRTVAAPSVFIFPPSDEQLSKGTASVVCLLNNFYPREAKVQWKVDNA 175

QY 180 LOSGNSQSVTEQDSKOSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 239  
 DB 176 LOSGNSQSVTEQDSKOSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 235  
 QY 240 C 240  
 DB 236 C 236  
 RESULT 6  
 Q6GMW0 HUMAN  
 ID Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6GMW0;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DE IGKV1-5 protein.  
 GN Name=IGKV1-5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Director MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073792; AAH73792.1; -; mRNA.  
 DR SNR; Q6GMW0; 21-233.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003066; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 235 AA; 25765 MW; 436C3686D4133F5 CRC64;  
 Query Match 78.6%; Score 977.5; DB 2; Length 235;  
 Best Local Similarity 78.8%; Pred. No. 1.1e-74;  
 Matches 190; Conservative 26; Mismatches 18; Indels 7; Gaps 2;  
 QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGRLVTLNCKSSQSLYSQGNQKNYLA 60

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Db 1 MEAPAQLLFLLWLLPDSSTGEIVMTQSPATLSVSPGERATLSCRASQSI-----SNLTA 54
QY 61 WYQKQPSQKLIYASARESGVPDRFSGSGGTDFTLTISSVQADVAIVYCOQYYS 120
Db 55 WYQQRFCQAPRLLIYAGSASRVGTGIPGRFSGSGGTDFTLTISSVQADVAIVYCOQYNDW 114
QY 121 PL-TFGAGTKLEKRTVAAPSVPFIFFPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 179
Db 115 LLVTFGQGTKEIKRTVAAPSVPFIFFPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 174
QY 180 LOSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNERGE 239
Db 175 LOSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNERGE 234
QY 240 C 240
Db 235 C 235

RESULT 7
Q6PJF2 HUMAN
ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSSP; P01837; IKCU.
DR SMR; Q6PJF2; 21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 77.9%; Pred. No. 1.1e-74;
Matches 187; Conservative 27; Mismatches 21; Indels 5; Gaps 1;

QY 1 MDSQAOVLMLLLWVSGTCGDIWVSQSPDSLAVSLGRVTLNCKSSQSLLYSGNKNVLA 60
Db 1 METPAQLFLLWLLPDSSTGEIVMTQSPATLSVSPGERATLSCRASQIV-----SSAYLA 55
QY 61 WYQKQPSQKLIYASARESGVPDRFSGSGGTDFTLTISSVQADVAIVYCOQYYS 120
Db 56 WYQKQPSQKLIYASARESGVPDRFSGSGGTDFTLTISSVQADVAIVYCOQYYS 115
QY 121 PL-TFGAGTKLEKRTVAAPSVPFIFFPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 180
Db 116 QGTFGQGTKEIKRTVAAPSVPFIFFPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 175
QY 181 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNERGE 240
Db 176 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNERGE 235

RESULT 8
Q8TCD0 HUMAN
ID Q8TCD0 HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSSP; P01837; IKCU.
DR SMR; Q8TCD0; 21-235.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
```

RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus  
 RT nephritis-associated idiotype.";  
 RL Nucleic Acids Res. 20:2601-0(1992).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1551402;  
 RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,  
 RA Thiebe R., Zocher I., Zachau H.G.;  
 RT "The human immunoglobulin kappa locus. Characterization of the  
 RT duplicated A regions.";  
 RL Eur. J. Immunol. 22:1023-1029(1992).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8258341;  
 RA Klein R., Jaenichen R., Zachau H.G.;  
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";  
 RL Eur. J. Immunol. 23:3248-3262(1993).  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation.";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 DR EMBL; BC022362; AAH22362.1; -; mRNA.  
 DR PIR; S22658; S22658.  
 DR PIR; S34095; S34095.  
 DR PIR; S40324; S40324.  
 DR PIR; S40374; S40374.  
 DR PIR; S42267; S42267.  
 DR PIR; S42268; S42268.  
 DR HSSP; P01834; 1172.  
 DR SMR; Q87CD0; 21-237.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 239 AA; 26235 MW; FAGEDCA3B03871D CRC64;  
 Query Match 78.6%; Score 976.5; DB 2; Length 239;  
 Best Local Similarity 80.2%; Pred. No. 1.4e-74;  
 Matches 190; Conservative 22; Mismatches 22; Indels 3; Gaps 2;  
 QY 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGSRVTLNCKSSQSLIYS-GNKNYLAWYQ 63  
 Db 5 AQLGLLLMLVPGSSGDVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGN--TYLWFPQ 62  
 QY 64 QKPGQSPKLLIYWASARESGVPRFSGSGGTDTFTLTISVQAEADVAVYCOQYSPILT 123  
 Db 63 QRPGQSPRLIYKVSNRDSGVPRFSGSGGTDTFTLTITRVEADVGVYCMQGTWHPST 122  
 QY 124 FGAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 183  
 Db 123 FGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 182  
 QY 184 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
 Db 183 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 9  
 Q6P588 HUMAN  
 ID Q6P588 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6P588;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Glandular pool- thyroid;  
 RP Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062704; AAH62704.1; -; mRNA.  
 DR HSSP; P01837; 1KCU.  
 DR SMR; Q6P588; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25773 MW; 953B37BEB4FF5F27 CRC64;  
 Query Match 78.4%; Score 975; DB 2; Length 236;  
 Best Local Similarity 77.6%; Pred. No. 1.8e-74;  
 Matches 187; Conservative 29; Mismatches 19; Indels 6; Gaps 2;  
 QY 1 MDSQAQVLMMLLLVSGTCGDIVMSQSPDSLAVSLGSRVTLNCKSSQSLIYSGNKNYLA 60  
 Db 1 METPAQLLLMLLMDTTGTEIVLTQSPGTLSPFSGERATLSCRASQTVFSS-----HLA 55  
 QY 61 WYQKQSPKLLIYWASARESGVPRFSGSGGTDTFTLTISVQAEADVAVYCOQYYSY 120  
 Db 56 WYQQRGPAPRLIYGAASRATGIPRFSGSGGTDTFTLTITRLEDFAVYFCQYGTGS 115  
 QY 121 P-LTFGAGTKLELKRITVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 179  
 Db 116 PSLTFGGGRFVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 175  
 QY 180 LOSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 239  
 Db 176 LOSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 235  
 QY 240 C 240



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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:18:02 ; Search time 20.202 Seconds  
(without alignments)  
1143.055 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAQVLMMLLLWVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	78.4	240	2 S06084	Ig kappa chain pre
2	972	78.2	216	2 JE0241	Ig kappa chain Am3
3	936.5	75.3	215	2 JE0242	Ig kappa chain NIG
4	926.5	74.5	215	2 JE0244	Ig kappa chain NIG
5	894.5	72.0	215	2 A23746	Ig kappa chain V-I
6	887.5	71.4	215	2 JE0243	Ig kappa chain NIG
7	833	67.0	220	2 A31790	Ig kappa chain V r
8	800	64.4	214	2 S68212	Ig kappa chain (Ma
9	757.5	60.9	225	2 S37484	Ig kappa chain - m
10	737	59.3	234	2 S14237	Ig kappa chain pre
11	728.5	58.6	219	2 S38865	Ig kappa chain - m
12	727.5	58.5	219	2 S52028	Ig kappa chain - m
13	727.5	58.5	230	2 S33161	Ig kappa chain - s
14	725.5	58.4	217	2 S42772	Ig kappa chain - m
15	724.5	58.3	219	2 PC4203	Ig kappa chain (mo
16	722	58.2	218	2 S68241	Ig kappa chain V r
17	722	58.1	218	2 JC5810	monoclonal antibod
18	718.5	57.8	219	2 S16112	Ig kappa chain V r
19	718	57.8	234	2 S01320	Ig kappa chain pre
20	700.5	56.4	235	2 S25058	Ig kappa chain - m
21	696.5	56.0	225	2 JL0029	Ig kappa chain pre
22	675	54.3	210	2 A56169	Ig kappa chain V r
23	662	53.3	145	2 PL0014	Ig kappa chain pre
24	633	50.9	178	2 PT0219	Ig kappa chain V-C
25	619	49.8	138	2 S26040	Ig kappa chain pre
26	614	49.4	134	2 PC1214	Ig kappa chain pre
27	613.5	49.4	197	2 S29593	Ig kappa chain (WM
28	595	47.9	135	2 S52059	JC-kappa protein -
29	595.5	47.1	238	2 A49633	Ig lambda-like cha

ALIGNMENTS

RESULT 1

S06084  
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C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C;Accession: S06084  
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDN  
A;Reference number: S06084; MUID:90016888; PMID:2508087  
A;Accession: S06084  
A;Molecule type: mRNA  
A;Residues: 1-240 <CRO>  
A;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:956457; PIDN:CAA34256.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-240/Product: Ig kappa chain #status predicted <MAT>  
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 975; DB 2; Length 240;

Best Local Similarity 76.2%; Pred. No. 4.2e-60;  
Matches 183; Conservative 20; Mismatches 37; Indels 0; Gaps 0;

Qy	1	MDSQAQVLMMLLLWVSGTCGDIWMSQSPDSLAVSLGERTVLTNCKSSQSLYSQGNQNYLA	60
Db	1	MESQTQVLSLLWISGTCGDFVMTQSPSLAVSAGETVTINCKSSQSLFYSQGNQNYLA	60
Qy	61	WYQQKPGSQPKLLIYWASARESGVPRFSGSGTGDTFTLTISVQAEADVYYCQYYSY	120
Db	61	WYQQKPGSQPKLLIYWASTRQSGVPRFSGSGTGDTFTLTISVQAEADLAIIYCLQYET	120
Qy	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQVKVNAL	180
Db	121	PYTFGAGTKLEKLRADAAPTVIFPPSTEQALATGGASVCLIMNFIYPRDISVKNKIDGTE	180
Qy	181	QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC	240
Db	181	RRDGVLDSTVDQDSKDSTYSMSSTLSLSKADYESHNLTYTCEVHVKTSSTSPVVKSFNRNEC	240

RESULT 2

JE0241  
Ig kappa chain Am37 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C;Accession: JE0241  
R;Alim, M.A.; Yanaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,  
submitted to JIPID, November 1998  
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu  
A;Reference number: JE0241  
A;Accession: JE0241



RESULT 8  
S68212  
IG kappa chain (Mab03-1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jan-2000  
C;Accession: S68212  
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T  
FEBS Lett. 375, 273-276, 1995  
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A;Reference number: S68211; MUID:96085223; PMID:7498516  
A;Accession: S68212  
A;Status: preliminary; nucleic acid sequence not shown

A; Residues: 1-214 <TAK>  
A; Cross-references: UNIPARC:UPI000017697E; EMBL:D29668  
C; Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match	64.4%	Score	800;	DB	2;	Length	214;
Best Local Similarity	70.1%;	Pred. No.	3.88-48;				
Matches	150;	Conservative	29;	Mismatches	35;	Indels	0;
						Gaps	0;

Qy	21	DI	V	M	S	O	S	P	D	S	L	A	V	S	G	E	R	V	T	L	N	C	K	S	O	S	L	L	Y	S	G	N	K	N	L	A	W	Q	O	K	P	C	S	P	K	L	L	I	Y	A	S	A	R	80
Db	1	D	I	V	M	T	S	P	S	S	L	A	M	S	V	G	O	K	V	T	M	S	C	K	S	Q	S	L	N	S	R	N	Q	N	L	A	W	Q	O	K	P	C	S	P	K	L	L	I	Y	A	S	T	R	60

Qy	81	ESGVDPDRSGSGGTFTLTLSVQAEDAVYCCOYYSYPLTFGAGTKLEIKRTVAAPS	140
Db	61	ESGVDPDRIGSGSGTFTLTSTVQAEDADYFCOOHYSTPTFFGGTKLSIKRADAAPT	120

Qy	141	VFI	P	P	S	D	E	O	L	K	G	T	A	S	V	C	L	N	N	P	P	R	E	A	K	V	Q	H	K	V	D	N	A	L	O	G	N	S	O	E	S	V	T	E	Q	D	S	K	D	S	T	S		200
Db	121	V	S	I	F	P	P	S	S	E	Q	L	T	G	G	A	S	W	C	F	L	N	P	P	K	I	D	G	S	E	R	Q	V	N	L	S	T	Q	D	S	K	D	S	T	S		180							

Qy	201	LSSTLTLSKADYEKHVYACEVTHOGLSPVTKS	234
		:     : : : : : : : : : : : : : :	
Db	181	MSSTLTTLTKDEYRHSNYTCEATHKSTSPVTKS	214

```

RESULT 9
S37484
IG kappa chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C/Accession: S37484
R/Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A/Reference number: S37483
A/Accession: S37484
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-225 <DUC>

```

**A;**Cross references: UniProtKB:Q90608; UniProtKB: Q90609; UniProtKB: P07354; UniProtKB: P07355; UniProtKB: P07356  
**B;**Superfamily: immunoglobulin V region; immunoglobulin homology  
**C;**Keywords: heterotrimer; immunoglobulin

	Indels	Mismatches	Gaps
Query Match	60.4%	60.4%	60.4%
Best Local Similarity	33.4%	33.4%	33.4%
Matches	147	147	147
Mismatches	32	32	32
Gaps	7	7	7

QY ..... 5  
DB 1 VFLLLCVSGAGHSIVNTQTPKFLLSAGDRVTITCKASQSV-----SNDVAVYQOKPGQ 54

55 SPKLLIYASSRYTGVPRDTGSGYGTDFFTISTVQAEDLAVYFCQDDYS-SYTFGGGT 113

129 **QY** **U** **L** **E** **K** **R** **A** **D** **A** **A** **P** **T** **S** **I** **F** **P** **P** **S** **S** **E** **Q** **L** **T** **S** **G** **G** **A** **S** **V** **C** **L** **N** **N** **F** **P** **K** **D** **I** **N** **V** **K** **W** **K** **I** **D** **S** **E** **R** **Q** **N** **G** **V** **L** **N** **S** 173

189 VTEQSDSTVYSLSSLTLTISKADVEHKVYACEVTHOGLSSPVTKSFNRGEC 240



**This Page Blank (uspto)**

Db 1 QLLGLLLWLLPGARCDIQVTQSPSSLSASLTERVSITCRTSQSV-----SNVLNMYQQ 54  
QY 65 KPGQSPKLLIYWASARESVPDRPSGSGSGTDFTLTISVQAEADVAVYYCOQYYSYPLTF 124  
Db 55 KPGQAPKLLIYYATRLTDVPSRPSGSGSGTDYTLTISNLEANDTATYYCLOYESTPLAF 114  
QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGN 184  
Db 115 GGTNVEIKSDQPSVFLPKPSEEQRLRTGTVSVCLVNDYFPKDINVKVKDGVTONSN 174  
QY 185 SQSVTEQDSKSTYSLSSTLTISKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 175 FONSFTDQDSKSTYSLSSTLTLSSEYQSHNAVACEVSHKSLPTALVKSFNRNEC 230  
RESULT 14  
S42772  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42772  
R:Schellekens, G.A.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S42771  
A:Accession: S42772  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SCH>  
A:Cross-references: UNIPARC:UPI00001161CD; EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PT  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:14-93/Domain: immunoglobulin homology <IMM>  
Query Match 58.4%; Score 725.5; DB 2; Length 217;  
Best Local Similarity 63.3%; Pred. No. 5.1e-43;  
Matches 138; Conservative 31; Mismatches 48; Indels 1; Gaps 1;  
QY 23 VMSQSPDSLAVSLGERVTLNCKSSQSLYSQNKNYLAWYQKPGQSPKLLIYWASARES 82  
Db 1 VMTQSPSLPVSIGDQASISCRSSQSLVHT-NGNTYLHWYLQKPGQSPKLLIYKVSTRFS 59  
QY 83 GVPDRFSGSGGTDFLTITISVQAEADVAVYYCOQYYSYPLTFGAGTKLELKRRTVAAPSVF 142  
Db 60 GVPDRFSGSGGTDFTFKISRVEAEDLGIVFCQSTVPTFTFGSGTKLEIKRADAAPTVS 119  
QY 143 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 202  
Db 120 IFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYMS 179  
QY 203 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 180 STLTLDKDEYERHNSYTCETHTKTSTSPIVKSFNRGEC 217

RESULT 15  
PC4203  
Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C:Accession: PC4203  
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.  
Gene 173, 257-259, 1996  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m  
A:Reference number: PC4202; MUID:97082978; PMID:8964510  
A:Accession: PC4203  
A:Molecule type: mRNA  
A:Residues: 1-219 <KWA>  
A:Cross-references: UNIPARC:UPI00001157E4; GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID  
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-112/Domain: V region #status predicted <VRG>  
F:113-219/Domain: C region #status predicted <CRG>

Query Match 58.3%; Score 724.5; DB 2; Length 219;  
Best Local Similarity 62.7%; Pred. No. 6e-43;  
Matches 138; Conservative 32; Mismatches 49; Indels 1; Gaps 1;  
QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSQNKNYLAWYQKPGQSPKLLIYWASAR 80  
Db 1 DVLMTQTPLSLPVSIGDQASISCRSSQSI VHT-NGNTYLEWYLQKPGQSPKLLIYKVSNR 59  
QY 81 ESGVPRDRFSGSGGTDFLTITISVQAEADVAVYYCOQYYSYPLTFGAGTKLELKRRTVAAPS 140  
Db 60 FSGVPRDRFSGSGGTDFLTIKISRVEAEDLGIVYFCQSGSHVPTFTFGGTTKLEIKRADAAPT 119  
QY 141 VFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 200  
Db 120 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSY 179  
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
Db 180 MSSTLTLTLDKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 219

Search completed: February 16, 2006, 10:23:49  
Job time : 21.202 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February '16, 2006, 10:12:02 ; Search time 132.121 Seconds  
(without alignments)  
798.138 Million cell updates/sec

Title: US-10-058-069-9  
Perfect score: 1243  
Sequence: 1 MDSQAVMLLLWVSGTGG.....EVTHQGLSSPVTKSFRNGEC 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing, first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	240	5	Aae27927 Human CC4
2	1243	100.0	240	6	Abb82836 Antibody
3	1166	93.8	240	2	Aay50156 Chimeric
4	1140	91.7	220	9	Adw77046 Light cha
5	1140	91.7	220	9	Adw44589 Antibody
6	1136	91.4	240	2	Aay50161 Human res
7	1135	91.3	220	9	Adw77054 Light cha
8	1132	91.1	240	9	Adw23408 Human L61
9	1132	91.1	240	9	Adz51047 Amino aci
10	1132	91.1	240	9	Adz56181 Protein s
11	1127.5	90.7	241	9	Adw23426 Human L55
12	1125.5	90.5	239	9	Adv92470 SW5-1 chl
13	1125.5	90.5	239	9	Adv98533 Novel chl
14	1125	90.5	240	4	Aau00815 Human Imm
15	1122	90.3	240	8	Adj65029 Plasmid p
16	1120.5	90.1	241	2	Aar28809 Vector pM
17	1119.5	90.1	241	9	Aeb45897 Human mon
18	1115	89.7	240	9	Aea41033 Human mon
19	1105.5	88.9	241	9	Aeb45859 Human mon
20	1090	87.7	244	3	Aay96305 Human IGF
21	1082	87.0	220	8	Adk52314 Human ant
22	1072.5	86.3	238	8	Adl23055 Humanised
23	1072.5	86.3	238	8	AdS88804 Humanised
24	1070	86.1	220	2	Aay50172 Antibody

ALIGNMENTS

RESULT 1  
AAE27927

ID AAE27927 standard; protein; 240 AA.

XX AAE27927;

XX 27-DEC-2002 (first entry)

XX Human CC49 antibody light chain protein.

XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.

XX Homo sapiens.

XX WO200260955-A2.

XX 08-AUG-2002.

XX 29-JAN-2002; 2002WO-US002373.

XX 29-JAN-2001; 2001US-0264318P.

PR 16-NOV-2001; 2001US-0331481P.

(IDEC-) IDEC PHARM CORP.

PI Braslawsky GR, Hanna N, Chinn P;

DR WPI; 2002-698547/75.

DR N-PSDB; AAD45756.

PT Novel domain deleted CC49 antibody reactive with tumor associated antigen  
-72, or C2B8 antibody reactive with CD20, useful for treating  
PT myelosuppressed patient suffering from a neoplastic disorder.

XX Example 1; Fig 5A; 74pp; English.

CC The present invention relates to domain deleted CC49 or C2B8 antibodies.  
CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain  
CC deleted sequence in which CH2 domain has been deleted and are reactive  
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive  
CC with CD20 and comprise a heavy chain having a sequence of a derived  
CC domain deleted C2B8 construct where the CH2 domain has been deleted.  
CC Sequences of the invention are useful for imaging a neoplasm. They are  
CC also useful for treating myelosuppressed patients suffering from  
CC neoplastic disorder such as haematologic neoplasm, preferably non-

CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
CC useful for reducing tumour size, inhibiting tumour growth and/or  
CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CC49 light chain protein. This  
CC sequence is used in the exemplification of the invention  
XX

SQ Sequence 240 AA;  
Query Match 100.0%; Score 1243; DB 5; Length 240;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSQAQVLMILLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60  
DB 1 MDSQAQVLMILLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGDTFTLTISVQAEDVAVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGDTFTLTISVQAEDVAVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 2  
ABB82836  
ID ABB82836 standard; protein; 240 AA.  
XX ABB82836;  
XX AC  
XX 31-MAR-2003 (first entry)  
XX DE Antibody huCC49 light chain.

XX CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thymometric; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.

XX OS Homo sapiens.  
XX PN WO200296948-A2.  
XX XX  
XX PD 05-DEC-2002.  
XX PF 29-JAN-2002; 2002WO-US002374.  
XX PR 29-JAN-2001; 2001US-0264318P.  
XX PR 16-NOV-2001; 2001US-0331481P.  
XX PR 21-DEC-2001; 2001US-0341858P.

XX (IDEC-) IDEC PHARM CORP.  
XX XX  
XX PI Braislawaky GR, Hanna N, Chinn P, Hariharan K;  
XX DR WPI; 2003-140446/13.  
XX DR N-PSDB; AB224020.

XX Novel dimeric antibody useful for treating immune disorder and neoplastic  
PT disorder, has several non-covalently associated monomeric subunits.

XX Example 1; Fig 5A; 78pp; English.  
XX The invention relates to a dimeric antibody (I) comprising several  
XX monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC

CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
XX represents the antibody huCC49 light chain

SQ Sequence 240 AA;  
Query Match 100.0%; Score 1243; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSQAQVLMILLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60  
DB 1 MDSQAQVLMILLWVSGTCGDI VMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGDTFTLTISVQAEDVAVYCCQYYSY 120  
DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGDTFTLTISVQAEDVAVYCCQYYSY 120  
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDSYLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 3  
AAY50156  
ID AAY50156 standard; protein; 240 AA.  
XX AAY50156;  
XX AC  
XX 17-OCT-2003 (revised)  
XX DT 31-JAN-2000 (first entry)  
XX DE Chimeric mouse/human F19 antibody light chain.

XX XX  
KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; chimeric; light chain.

XX OS Mus sp.  
XX OS Homo sapiens.  
XX OS Chimeric.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..20 /note= "Leader peptide"  
XX FT Protein 21..240 /note= "Mature chimeric mouse/human F19 light chain"  
XX FT Region 21..140 /note= "Mature mouse F19 light chain variable region"  
XX FT Region 44..60 /note= "Complementarity determining region (CDR) 1"  
XX FT Region 76..82 /note= "CDR 2"  
XX FT Region 115..123 /note= "CDR 3"  
XX FT Region 141..240





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XX SQ Sequence 220 AA;
Query Match 91.7%; Score 1140; DB 9; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.1e-61;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 60

QY 81 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120

QY 141 VFIFPPSDEQLKSGTASVVCLLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKDYTS 200
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKDYTS 180

QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 5
ADW44589
ID ADW44589 standard; protein; 220 AA.
XX AC ADW44589;
XX DT 24-MAR-2005 (first entry)
XX DE Antibody huCC49 light chain (CH2 domain deleted).
KW Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;
KW Antinflammatory; Gastrointestinal-Gen.; Dermatological; Antiulcer;
KW Antirheumatic; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;
KW huCC49; Tag72; light chain variable region.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX WO2005000899-A2.
XX PD 06-JAN-2005.
XX PF 28-JUN-2004; 2004WO-US020945.
XX PR 27-JUN-2003; 2003US-0483877P.
XX PR 03-OCT-2003; 2003US-0508810P.
XX PR 28-OCT-2003; 2003US-0515311P.
XX PR 30-OCT-2003; 2003US-0516030P.
XX PA (BIOG-) BIOGEN IDEC MA INC.
XX GLaser S, Reff M, Yang T, Wu X, Chinn P;
XX WPI: 2005-058133/06.
XX N-PSDB; ADW44586.
XX New composition comprising polypeptide dimers comprising at least four
XX binding sites and at least two polypeptide chains linked via at least one
XX interchain disulfide linkage, useful for treating e.g., cancer or
XX autoimmune diseases.
XX Claim 35; SEQ ID NO 21; 172pp; English.
XX The invention relates to a composition comprising polypeptide dimers
XX comprising at least four binding sites and at least two polypeptide

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CC chains, where the polypeptide chains comprise at least one heavy chain
CC portion and a synthetic connecting peptide, and where greater than about
CC 50% of the dimers comprise polypeptide chains that are linked via at
CC least one interchain disulfide linkage, or comprising minibody molecules
CC comprising two polypeptide chains, where the polypeptide chains comprise
CC a heavy chain portion and a synthetic connecting peptide, where the
CC polypeptide chains lack all or part of a CH2 domain, and where greater
CC than about 50% of the molecules are present in a form in which one of the
CC polypeptide chains are linked via at least one interchain disulfide
CC linkage. Also included are a nucleic acid molecule comprising a
CC nucleotide sequence encoding a polypeptide chain as defined above, a host
CC cell comprising a vector and a binding molecule comprising CH2 deleted
CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p3E8. The
CC synthetic connecting peptide comprises a (Gly-Ser)n linker attached to a
CC portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are
CC bispecific and comprise at least one binding site specific for a soluble
CC ligand or for a cell surface molecule. The molecules comprise two binding
CC sites specific for a tumor cell antigen and two binding sites specific
CC for a prodrug. The synthetic connecting peptide comprises a proline
CC residue at position 243. Kabat numbering system. The synthetic connecting
CC peptide further comprises an alanine residue at position 244 and a
CC proline residue at position 245, Kabat numbering system. The polypeptide
CC dimers are tetraivalent minibody molecules. The composition is useful for
CC treating a subject that would benefit from treatment with an antigen
CC binding molecule, where the subject is suffering from cancer, lymphoma,
CC an autoimmune disease or disorder, or an inflammatory disease or disorder
CC The composition is useful for treating autoimmune diseases such as
CC Crohn's disease, inflammatory bowel disease, systemic lupus
CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's
CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,
CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious
CC anemia, Sjogren's syndrome, neurological disorders such as multiple
CC sclerosis, and inflammatory diseases or disorders such as cystic
CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The
CC polypeptide is useful for diagnostic or therapeutic purposes. The binding
CC molecules are also useful for pretargeting applications for
CC chemotherapeutic drug delivery. The present sequence represents a light
CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72
XX antibody huCC49.
SQ Sequence 220 AA;
Query Match 91.7%; Score 1140; DB 9; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.1e-61;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKYNLAWYQKPGQSPKLLIYWASAR 60

QY 81 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVDPDRFSGSGGTDFTLTISVVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120

QY 141 VFIFPPSDEQLKSGTASVVCLLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKDYTS 200
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKDYTS 180

QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

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```

RESULT 6
ADW50161
ID AAY50161 standard; protein; 240 AA.
XX AC AAY50161;
XX DT 17-OCT-2003 (revised)
XX DT 31-JAN-2000 (first entry)
XX DE Human reshaped F19 antibody light chain (version a).

```



PS Claim 31; SEQ ID NO 27; 152pp; English.

XX The invention relates to a composition comprising polypeptide dimers

CC having at least two binding sites and at least two polypeptide chains,

CC where the polypeptide chains comprise at least one heavy chain portion

CC and a synthetic connecting peptide. The invention also relates to a

CC nucleic acid molecule comprising a nucleotide sequence encoding a

CC polypeptide chain, a host cell comprising the nucleic acid molecule, a

CC connecting peptide, a domain deleted antibody molecule, an antibody

CC molecule, a method of separating a first properly folded antibody

CC molecule from a second improperly folded antibody molecule, where each of

CC the first and second antibody molecules comprises four polypeptide

CC chains, where at least two of the chains comprise at least one heavy

CC chain portion, and at least two of the chains comprise at least one light

CC chain portion, a method of increasing the amount of a first polypeptide

CC dimer relative to the amount of a second polypeptide dimer produced by a

CC cell, a composition comprising a first polypeptide dimer, a polypeptide

CC comprising a synthetic connecting peptide, where the polypeptide is not a

CC naturally occurring IgG3 molecule, and a method of increasing the amount

CC of dimers comprising polypeptide chains linked via at least one disulfide

CC linkage in a population of IgG4 molecules produced by a cell. The

CC composition is useful for treating a subject that would benefit from

CC treatment with a binding molecule, where the subject is suffering from

CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory

CC disease or disorder. The autoimmune diseases include Crohns disease,

CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative

CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,

CC Hashimoto's disease, pemphigus vulgaris, myasthenia gravis, scleroderma,

CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.

CC This sequence represents a light chain CH2 domain-deleted hucC49

CC polypeptide, used in the scope of the invention.

XX

SQ Sequence 220 AA;

Query Match 91.3%; Score 1135; DB 9; Length 220;

Best Local Similarity 99.5%; Pred. No. 1.2e-60;

Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 DIVMSGPSPLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQPKLLIYWASAR 80

DB 1 DIVMSGPSPLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQPKLLIYWASAR 60

QY 81 ESGVDPFRSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140

DB 61 ESGVDPFRSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRITVAAPS 120

QY 141 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 200

DB 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 180

QY 201 LSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

DB 181 LSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 8

ADW23408

ID ADW23408 standard; protein; 240 AA.

XX ADW23408;

AC ADW23408;

DT 07-APR-2005 (first entry)

XX Human L612L protein.

DE

XX immunoglobulin M; IgM; IgM H chain; IgM L chain; IgM J chain;

KW immunostimulatory; cytostatic; anti-HIV; cancer;

KW acquired immunodeficiency syndrome; L612L.

XX Homo sapiens.

OS

XX WO2005005636-A1.

PN

XX

PD 20-JAN-2005.

XX

PF 15-JUL-2004; 2004WO-JP010444.

XX

PR 15-JUL-2003; 2003US-0487333P.

XX

PA (CHUS ) CHUGAI SEIYAKU KK.

PA (IRIE/) IRIE R.

PI Irie R, Teunoda H, Igawa T, Sekimori Y, Tsuchiya M;

DR WPI; 2005-122424/13.

XX N-PSDB; ADW23407.

XX New transformed Chinese hamster ovarian cell producing a specific amount

PT of immunoglobulin M, for use in treating a tumor or acquired

PT immunodeficiency syndrome.

XX

PS Claim 35; SEQ ID NO 4; 132pp; Japanese.

XX This invention describes a novel method for producing a transformed cell

CC capable of producing 100 mg/l or 35 or more pg/cell/day of immunoglobulin

CC M (IgM). Pentamer IgM is obtained by locating the IgM H chain, L chain or

CC J chain on a single vector and transforming the vector into an

CC appropriate host cell from a mammalian cell line. Substantially pure IgM

CC is obtained by purifying IgM from the culture supernatant of the cell

CC culture product. The gene encoding the J chain may be transferred via

CC cotransformation. If the J chain is not expressed the product is obtained

CC as hexamer IgM. The transformant obtained shows a high IgM productivity.

CC The invention also describes a method whereby a polymer IgM can be

CC separated and quantified. The products of the invention are

CC immunostimulatory and have cytostatic and anti-HIV activity. The purified

CC IgM can be used to treat or prevent cancer or acquired immunodeficiency

CC syndrome (AIDS). This sequence represents the human IgM associated

CC polypeptide, L612L.

XX

SQ Sequence 240 AA;

Query Match 91.1%; Score 1132; DB 9; Length 240;

Best Local Similarity 91.1%; Pred. No. 2e-60;

Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 QAOVLMLLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQ 63

DB 4 QTOVFISLLLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 63

QY 64 QKPGQPKLLIYWASARESGVDPFRSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSYPLT 123

DB 64 QKPGQPKLLIYWASTRESGVDPFRSGSGGTDFTLTITSSVQAEADVAVVYCCQYYSYPT 123

QY 124 FGAGTKLELKRITVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183

DB 124 FGQGTKEIKRTVAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183

QY 184 NSQESVTEQDSKDSSTYSLSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

DB 184 NSQESVTEQDSKDSSTYSLSSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 9

ADZ51047

ID ADZ51047 standard; protein; 240 AA.

XX ADZ51047;

XX

DT 30-JUN-2005 (first entry)

XX Amino acid sequence of protein #2.

DE

XX immunoglobulin M; IgM; multi-valent cationic ion; Magnesium chloride;

KW arginine hydrochloride.

XX

OS Unidentified.

```
XX PN WO2005035574-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP014935.
XX PR 09-OCT-2003; 2003JP-00351388.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Igawa T, Sekimori Y;
XX WPI; 2005-315547/32.
XX DR N-PSDB; ADZ51046.
XX PT Stabilized solution, useful for preparing a stable pharmaceutical
XX PT composition containing immunoglobulin (IgM, comprises a high
XX PT concentration of immunoglobulin IgM.
XX PS Example 6; SEQ ID NO 4; 44pp; Japanese.
XX CC The specification describes a stabilized solution of high concentration
XX CC immunoglobulin M (IgM). The use of a multi-valent cationic ion, such as
XX CC Magnesium chloride or arginine hydrochloride, as an additive allows
XX CC inhibition of the association of IgM in a solution. The present sequence
XX CC represents a protein, and is used in the course of the invention.
XX SQ Sequence 240 AA;
XX Query Match 91.1%; Score 1132; DB 9; Length 240;
XX Best Local Similarity 91.1%; Pred. No. 2e-60;
XX Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
XX QY 4 QRAQLMLLLVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLYSNGNKNYLAWYQ 63
XX DB 4 QTVFISLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQ 63
XX QY 64 QKPGQPKLLIYWASARESGVDPFRFSGSGTDFTLTISSVQAEADVAVYCCQYYSTPPT 123
XX DB 64 QKFGQPKLLIYWASTRESGVDPFRFSGSGTDFTLTISSLQAEADVAVYCCQYYSTPPT 123
XX QY 124 FGAGTKLEKRTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
XX DB 124 FGQGTKEIKRTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
XX QY 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGC 240
XX DB 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGC 240
XX RESULT 10
XX ID ADZ56181 standard; protein; 240 AA.
XX AC ADZ56181;
XX DT 30-JUN-2005 (first entry)
XX DE Protein stabilization method-related protein - SEQ ID 4.
XX KW protein stabilization; pharmaceutical.
XX OS Unidentified.
XX PN WO2005035573-A1.
XX PD 21-APR-2005.
XX PF 08-OCT-2004; 2004WO-JP014919.
XX PR 09-OCT-2003; 2003JP-00351410.
XX PI Irie R, Tsunoda H, Igawa T, Sekimori Y, Tsuchiya M;
XX XX
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PA (CHUS ) CHUGAI SEIYAKU KK.
XX Hayasaka A, Igawa T, Sekimori Y;
XX WPI; 2005-315546/32.
XX DR N-PSDB; ADZ56180.
XX PT Stabilizing IgM protein from low temperature precipitation, by adding
XX PT citrate buffer solution to solution containing protein.
XX PS Example 3; SEQ ID NO 4; 31pp; Japanese.
XX CC The invention comprises a method of stabilizing a protein from a low
XX CC temperature precipitation, the method involves adding citrate buffer to
XX CC the solution containing the protein. The method of the invention is
XX CC useful for stabilizing protein from a low temperature precipitation and
XX CC in producing stable pharmaceutical compositions containing IgM. The
XX CC present amino acid sequence represents a protein that was used in an
XX CC example of the invention. NOTE: The present sequence is not shown in the
XX CC specification, but has been retrieved from the WIPO website.
XX SQ Sequence 240 AA;
XX Query Match 91.1%; Score 1132; DB 9; Length 240;
XX Best Local Similarity 91.1%; Pred. No. 2e-60;
XX Matches 216; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
XX QY 4 QRAQLMLLLVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLYSNGNKNYLAWYQ 63
XX DB 4 QTVFISLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNNKNYLAWYQ 63
XX QY 64 QKPGQPKLLIYWASARESGVDPFRFSGSGTDFTLTISSVQAEADVAVYCCQYYSTPPT 123
XX DB 64 QKFGQPKLLIYWASTRESGVDPFRFSGSGTDFTLTISSLQAEADVAVYCCQYYSTPPT 123
XX QY 124 FGAGTKLEKRTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
XX DB 124 FGQGTKEIKRTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
XX QY 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGC 240
XX DB 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGC 240
XX RESULT 11
XX ID ADW23426 standard; protein; 241 AA.
XX AC ADW23426;
XX DT 07-APR-2005 (first entry)
XX DE Human L55L protein.
XX KW immunoglobulin M; IgM; IgM H chain; IgM L chain; IgM J chain;
XX KW immunostimulatory; cytostatic; anti-HIV; cancer;
XX KW acquired immunodeficiency syndrome; L55L.
XX OS Homo sapiens.
XX PN WO2005005636-A1.
XX PD 20-JAN-2005.
XX PF 15-JUL-2004; 2004WO-JP010444.
XX PR 15-JUL-2003; 2003US-0487333P.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PA (IRIE/) IRIE R.
XX PI Irie R, Tsunoda H, Igawa T, Sekimori Y, Tsuchiya M;
XX XX
```

DR WPI: 2005-122424/13.  
 DR N-PSDB; ADW23425.  
 XX  
 PT New transformed Chinese hamster ovarian cell producing a specific amount  
 PT of immunoglobulin M, for use in treating a tumor or acquired  
 PT immunodeficiency syndrome.  
 XX  
 XX  
 PS Claim 42; SEQ ID NO 22; 132pp; Japanese.  
 XX  
 CC This invention describes a novel method for producing a transformed cell  
 CC capable of producing 100 mg/l or 35 or more pg/cell/day of immunoglobulin  
 CC M (IgM). Pentamer IgM is obtained by locating the IgM H chain, L chain or  
 CC J chain on a single vector and transforming the vector into an  
 CC appropriate host cell from a mammalian cell line. Substantially pure IgM  
 CC is obtained by purifying IgM from the culture supernatant of the cell  
 CC culture product. The gene encoding the J chain may be transferred via  
 CC cotransformation. If the J chain is not expressed the product is obtained  
 CC as hexamer IgM. The transformant obtained shows a high IgM productivity.  
 CC The invention also describes a method whereby a polymer IgM can be  
 CC separated and quantified. The products of the invention are  
 CC immunostimulatory and have cytostatic and anti-HIV activity. The purified  
 CC IgM can be used to treat or prevent cancer or acquired immunodeficiency  
 CC syndrome (AIDS). This sequence represents the human IgM associated  
 CC polypeptide, L55L.  
 XX  
 SQ Sequence 241 AA;

Query Match 90.7%; Score 1127.5; DB 9; Length 241;  
 Best Local Similarity 90.8%; Pred. No. 3.7e-60;  
 Matches 216; Conservative 9; Mismatches 12; Indels 1; Gaps 1;  
 QY 4 QAOVLMLLLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 63  
 DB 4 QTVQVFLSLWTSGAYGDIWMTQSPDSLAVSLGERATINCKSSQSLYSSNNKNYLA 63  
 QY 64 QKPGQSPKLLIYWASARESGVDPDRFGSGSGTDFTLTISVQAEDEVAVYVCOQY-SYPL 122  
 DB 64 QKPGQSPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLQAEDEVAVYVCOQYITLPL 123  
 QY 123 TFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQS 182  
 DB 124 TFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQS 183  
 QY 183 GNSQESVTEQDSKDYSLSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240  
 DB 184 GNSQESVTEQDSKDYSLSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 12  
 ADV92470  
 ID ADV92470 standard; protein; 239 AA.  
 XX  
 AC ADV92470;  
 XX  
 XX 10-MAR-2005 (first entry)  
 XX  
 DE SM5-1 chimeric antibody (ChSM) light chain protein.  
 XX  
 KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
 KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
 KW breast cancer; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= Signal peptide  
 FT 21..239  
 FT Protein /note= "Mature SM5-1 chimeric antibody (ChSM) light chain  
 FT protein"  
 FT 21..133  
 FT Region

FT Region /note= "Light chain variable region gene (VL)"  
 FT 134..239  
 FT /note= "Human kappa chain constant cDNA (CL)"  
 XX  
 PN US2004254108-A1.  
 XX 16-DEC-2004.  
 XX  
 XX 26-NOV-2003; 2003US-00723003.  
 XX  
 PR 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 XX  
 PA (MAJJ/) MA J.  
 PA (GUOY/) GUO Y.  
 XX  
 PI Ma J, Guo Y;  
 XX WPI: 2005-030218/03.  
 DR N-PSDB; ADV92469.  
 XX  
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 PS Example 3; SEQ ID NO 14; 158pp; English.  
 XX  
 CC The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the SM5-1 chimeric antibody (ChSM)  
 CC light chain protein.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 90.5%; Score 1125.5; DB 9; Length 239;  
 Best Local Similarity 89.6%; Pred. No. 4.9e-60;  
 Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
 QY 1 MDSQAOVLMLLLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60  
 DB 1 MESQTOVFLSLLLWVSGTCGIMMTQSPDSLAVSAGEKVTMSCKSSQSLYSSNQKNYLA 60  
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFGSGSGTDFTLTISVQAEDEVAVYVCOQYYSY 120  
 DB 61 WYQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGTDFTLTISVQAEDEVAVYVCOQYYSY 119  
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180  
 DB 120 SYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 179  
 QY 181 QSGNSQESVTEQDSKDYSLSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240  
 DB 180 QSGNSQESVTEQDSKDYSLSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 13  
 ADV98533  
 ID ADV98533 standard; protein; 239 AA.  
 XX  
 AC ADV98533;  
 XX  
 XX 24-MAR-2005 (first entry)  
 XX  
 DE Novel chimeric protein-related ChSM light chain protein SeqID14.  
 XX  
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Mus sp.  
 OS Synthetic.



SQ Sequence 240 AA;  
Query Match 90.5%; Score 1125; DB 4; Length 240;  
Best Local Similarity 90.3%; Pred. No. 5.2e-60;  
Matches 214; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 4 QAOVLMLLLWVSGTCGDIWMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLA 63  
DB 4 QTVFISLLWTSYGADIVMTQSPDSLAVSLGERATINCKSQTVLYSSDNKNYLA 63  
QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVYCCOYYSYPLT 123  
DB 64 QKPGQSPKLLIYWASTRESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVYCCOYYSTPVS 123  
QY 124 FGAGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183  
DB 124 FQGGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183  
QY 184 NSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 184 NSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 15  
ADJ65029  
ID ADJ65029 standard; protein; 240 AA.  
AC ADJ65029;  
DT 06-MAY-2004 (first entry)  
XX Plasmid pD16-H39E3.L1 light chain antibody amino acid sequence SEQ:8.  
DE humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;  
KW gene therapy; antibody; plasmid; pD16-H39E3.L1.  
XX Synthetic.  
XX WO2004010947-A2.  
XX 05-FEB-2004.  
XX 30-JUL-2003; 2003WO-US023735.  
XX 30-JUL-2002; 2002US-0399646P.  
PR (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;  
PI Thorne B, Shuford WW, Mittler RS;  
XX WPI; 2004-143726/14.  
DR N-PSDB; ADJ65027.  
XX New humanized antibody that binds to human 4-1BB and allows binding of  
PT human 4-1BB to a human 4-1BB ligand, useful for preparing a composition  
PT for treating cancer.  
XX Claim 4; SEQ ID NO 8; 78pp; English.  
XX The present invention describes a humanised antibody (I) that binds to  
CC human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.  
CC Also described: (1) a pharmaceutical composition comprising the antibody  
CC (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated  
CC polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs  
CC (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-  
CC 1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic  
CC activity, and can be used in gene therapy. The humanised antibody (I) can  
CC be used for preparing a composition for treating cancer. The present  
CC sequence represents the plasmid pD16-H39E3.L1 light chain antibody amino  
CC acid sequence, which is used in an example from the present invention.  
XX Sequence 240 AA;

Query Match 90.3%; Score 1122; DB 8; Length 240;  
Best Local Similarity 90.0%; Pred. No. 7.9e-60;  
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MDSQAQVLMLLWVSGTCGDIWMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLA 60  
DB 1 MEAPAQLLFLLLLWLPDITGDIWMTQSPDSLAVSLGERATINCKSSQSLLYSGNQKNYLA 60  
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVYCCOYYSY 120  
DB 61 WYQKPGQSPKLLIYASTRQSGVDPDRFSGSGSGTDFLTITSSVQAEADVAVYCCOYYDRY 120  
QY 121 PLTFGAGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
DB 121 PFTFGGQTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180  
QY 181 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240  
DB 181 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

Search completed: February 16, 2006, 10:17:41  
Job time : 134.121 secs



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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:39:32 ; Search time 13.1111 Seconds  
(without alignments)  
383.795 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSLLFLVAVATRVLSQ.....MHEALHHYTKSLSLSPK 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_New.\*
- 1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1632	87.0	462	7	US-11-177-648-30 Sequence 30, Appl
2	1630	86.9	462	7	US-11-177-648-97 Sequence 97, Appl
3	1629	86.8	462	7	US-11-177-648-29 Sequence 29, Appl
4	1629	86.8	462	7	US-11-177-648-32 Sequence 32, Appl
5	1628	86.8	462	7	US-11-177-648-96 Sequence 96, Appl
6	1627	86.7	462	7	US-11-177-648-95 Sequence 95, Appl
7	1626	86.7	462	7	US-11-177-648-33 Sequence 33, Appl
8	1624	86.6	462	7	US-11-177-648-31 Sequence 31, Appl
9	1624	86.6	462	7	US-11-177-648-94 Sequence 94, Appl
10	1622	86.5	462	7	US-11-177-648-93 Sequence 93, Appl
11	1621	86.4	462	7	US-11-177-648-92 Sequence 92, Appl
12	1619	86.3	462	7	US-11-177-648-27 Sequence 27, Appl
13	1616	86.1	462	7	US-11-177-648-28 Sequence 28, Appl
14	1614	86.0	462	7	US-11-177-648-98 Sequence 98, Appl
15	1612	85.9	462	7	US-11-177-648-26 Sequence 26, Appl
16	1608	85.7	462	7	US-11-177-648-79 Sequence 79, Appl
17	1599	85.2	462	7	US-11-177-648-9 Sequence 9, Appl
18	1566.5	83.5	467	7	US-11-158-505-72 Sequence 72, Appl
19	1565.5	83.4	467	7	US-11-158-505-5 Sequence 5, Appl
20	1565.5	83.4	467	7	US-11-158-505-7 Sequence 7, Appl
21	1565.5	83.4	467	7	US-11-158-505-13 Sequence 13, Appl
22	1565.5	83.4	467	7	US-11-158-505-15 Sequence 15, Appl
23	1565.5	83.4	467	7	US-11-158-505-21 Sequence 21, Appl
24	1565.5	83.4	467	7	US-11-158-505-23 Sequence 23, Appl
25	1565.5	83.4	467	7	US-11-158-505-29 Sequence 29, Appl

## ALIGNMENTS

### RESULT 1

US-11-177-648-30  
; Sequence 30, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; CURRENT FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H15  
US-11-177-648-30

Query Match 87.0%; Score 1632; DB 7; Length 462;

Best Local Similarity 69.2%; Pred. No. 3.2e-97;

Matches 321; Conservative 10; Mismatches 21; Indels 112; Gaps 2;

QY	1	MGWSLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWMVKQP	60
Db	1	MGWSLLFLVATATGVHSGVQLVQSGAEVVKPGASVKISCKASGYTFTSYWHWVKQP	60
QY	61	QGRLEWIGVSPGNDFKYNERFKGKATLTADTSASTAYVELSSLRSDETAIVFCTRSLN	120
Db	61	QGRLEWIGVSPGNDFKYNERFKGKATLTADTSASTAYVELSSLRSDESAVYVC--ELG	118
QY	121	MAYWGQGLTVTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL	180
Db	119	QGYWGQGLTVTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL	178
QY	181	TSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTTQYICNVNHNKPSNTKVDKKVPKSCDKT	240
Db	179	TSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTTQYICNVNHNKPSNTKVDKKVPKSCDKT	238

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QY      241  HTCPCP----- 247
Db      239  HTCPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY      248  -----GQP 250
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQP 358
QY      251  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
QY      311  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 354
Db      419  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 462

RESULT 2
US-11-177-648-97
; Sequence 97, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H24
US-11-177-648-97

Query Match      86.9%; Score 1630; DB 7; Length 462;
Best Local Similarity 69.2%; Pred. No. 4.3e-97;
Matches 321; Conservative 8; Mismatches 23; Indels 112; Gaps 2;

QY      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60
Db      1  MGWSLILLFLVATATGVHSGVQLVQSGAEVVKPGASVKISCKASGYTFTSYNMHWYKQP 60
QY      61  GQRLIEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLSEDTAVYFCTRSLN 120
Db      61  GQGLEWIGNINPNSGGTNYNEKFKSRATLTTRDTSTSTAYMELSSLRSEDTAVYVC--ELG 118
QY      121  MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
Db      119  QGYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
QY      181  TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKVPEKSCDKT 240
Db      179  TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKVPEKSCDKT 238
QY      241  HTCPCP----- 247
Db      239  HTCPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY      248  -----GQP 250
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQP 358
QY      251  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
QY      311  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 354
Db      419  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 462

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Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQP 358
QY      251  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
QY      311  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 354
Db      419  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 462

RESULT 3
US-11-177-648-29
; Sequence 29, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H14
US-11-177-648-29

Query Match      86.8%; Score 1629; DB 7; Length 462;
Best Local Similarity 69.2%; Pred. No. 5e-97;
Matches 321; Conservative 9; Mismatches 22; Indels 112; Gaps 2;

QY      1  MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWYKQP 60
Db      1  MGWSLILLFLVATATGVHSGVQLVQSGAEVVKPGASVKISCKASGYTFTSYNMHWYKQP 60
QY      61  GQRLIEWIGYFSPGNDDFKYNRERFKGKATLTADTSASTAYVELSSLRSEDTAVYFCTRSLN 120
Db      61  GQGLEWIGNINPNSGGTNYNEKFKSRATLTTRDTSTSTAYMELSSLRSEDTAVYVC--ELG 118
QY      121  MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
Db      119  QGYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
QY      181  TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKVPEKSCDKT 240
Db      179  TSGVHTFPVAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKVPEKSCDKT 238
QY      241  HTCPCP----- 247
Db      239  HTCPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY      248  -----GQP 250
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQP 358
QY      251  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
QY      311  FFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 354

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Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 462

RESULT 4

US-11-177-648-32  
; Sequence 32, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; PRIOR FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H17  
US-11-177-648-32

Query Match 86.8%; Score 1629; DB 7; Length 462;

Best Local Similarity 69.2%; Pred. No. 5e-97;  
Matches 321; Conservative 8; Mismatches 23; Indels 112; Gaps 2;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60  
Db 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQRP 60  
QY 61 GQRLWIGVPSGNDDFKYNRPFKSKATLTADTSASTAYVELSSLRSEDYAVYFCTRSIN 120  
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSTSTAYMELSLRSEDYAVYIC--ELG 118  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
Db 119 QGWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
QY 181 TSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 240  
Db 179 TSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 238  
QY 241 HTCPPCP-----247  
Db 239 HTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298  
QY 248 -----GOP 250  
Db 299 VHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTIISKAKGQP 358  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 310  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 418  
QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 354  
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 462

RESULT 5

US-11-177-648-96  
; Sequence 96, Application US/11177648

; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS  
; FILE REFERENCE: PB60608-2  
; CURRENT APPLICATION NUMBER: US/11/177,648  
; PRIOR FILING DATE: 2005-07-06  
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
; PRIOR FILING DATE: 2004-12-20  
; PRIOR APPLICATION NUMBER: GB0329711.6  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: GB0329684.5  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 2A10 heavy chain humanised construct H23  
US-11-177-648-96

Query Match 86.8%; Score 1628; DB 7; Length 462;

Best Local Similarity 69.0%; Pred. No. 5.8e-97;  
Matches 320; Conservative 9; Mismatches 23; Indels 112; Gaps 2;

QY 1 MGSLLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60  
Db 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQRP 60  
QY 61 GQRLWIGVPSGNDDFKYNRPFKSKATLTADTSASTAYVELSSLRSEDYAVYFCTRSIN 120  
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSTSTAYMELSLRSEDYAVYIC--ELG 118  
QY 121 MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180  
Db 119 QGWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178  
QY 181 TSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 240  
Db 179 TSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKT 238  
QY 241 HTCPPCP-----247  
Db 239 HTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298  
QY 248 -----GOP 250  
Db 299 VHNAKTKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTIISKAKGQP 358  
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 310  
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 418  
QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 354  
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 462

RESULT 6

US-11-177-648-95  
; Sequence 95, Application US/11177648  
; Publication No. US20060029603A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonathon Henry ELLIS  
; APPLICANT: Paul Andrew HAMBLIN  
; APPLICANT: Paul Alexander WILSON  
; APPLICANT: Alan Peter LEWIS  
; TITLE OF INVENTION: IMMUNOGLOBULINS

```
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: 2A10 heavy chain humanised construct H22
US-11-177-648-95

Query Match      86.7%; Score 1627; DB 7; Length 462;
Best Local Similarity 69.0%; Pred. No. 6,7e-97;
Matches 320; Conservative 9; Mismatches 23; Indels 112; Gaps 2;

QY 1 MGSLLILFLVAVATRVLSQVLQVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGSLLILFLVATATGVHSQVLQVQSGAEVVKPGASVKISCKASGYTFISYWHWVKQP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GORLEWIGFSPGNDDFKYNRPFKSKATLTADTSATAYVELSSLRSEDATVYFCTRSLN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSSSTAYMELSLRSEDATVYVC--ELG 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 MAYWGGTILVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWSGAL 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 119 QGYWQGGLTVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWSGAL 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 179 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 HTCPPCP-----247
   |||||
Db 239 HTCPPCPAPELAGAPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
   |||||
QY 248 -----GOP 250
   |||||
Db 299 VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
   |||||
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
   |||||
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
   |||||

QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
   |||||
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462
   |||||

RESULT 7
US-11-177-648-33
; Sequence 33, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
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```
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H18
US-11-177-648-33

Query Match      86.7%; Score 1626; DB 7; Length 462;
Best Local Similarity 69.0%; Pred. No. 7,7e-97;
Matches 320; Conservative 10; Mismatches 22; Indels 112; Gaps 2;

QY 1 MGSLLILFLVAVATRVLSQVLQVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGSLLILFLVATATGVHSQVLQVQSGAEVVKPGASVKISCKASGYTFTSYWHWVKQP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GORLEWIGFSPGNDDFKYNRPFKSKATLTADTSATAYVELSSLRSEDATVYFCTRSLN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGNINPSNGGTNYNEKFKSKATLTVDKSSSTAYMELSLRSEDATVYVC--ELG 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 MAYWGGTILVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWSGAL 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 119 QGYWQGGLTVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWSGAL 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 179 TSGVHTFPVAVLQSSGLYSLSVVTVPPSSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 HTCPPCP-----247
   |||||
Db 239 HTCPPCPAPELAGAPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
   |||||
QY 248 -----GOP 250
   |||||
Db 299 VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
   |||||
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
   |||||
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
   |||||

QY 311 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
   |||||
Db 419 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 462
   |||||

RESULT 8
US-11-177-648-31
; Sequence 31, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
```



```
Db      61  GCGLEWIGNINPNSGGTNNEXFKSKATWTRDTSTSTAYWELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKOYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTPCPCP----- 247
      |||||
Db      239  HTPCPCPAPELAGAPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||
Qy      248  -----GQP 250
      |||||
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
      |||||
Qy      251  REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
      |||||
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
      |||||
Qy      311  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 354
      |||||
Db      419  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 462
      |||||
```

```
RESULT 11
US-11-177-648-92
; Sequence 92, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H19
US-11-177-648-92
```

```
Query Match      86.4%; Score 1621; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 1.6e-96;
Matches 318; Conservative 11; Mismatches 23; Indels 112; Gaps 2;

Qy      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWHYKQP 60
Db      1  MGWSLILLFLVATATGVHSGVQLVQSGAEVVKPGASVKISKASGYTFTSYNWHWYRQP 60
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      61  GORLEWIGYFSPGNDDFKYNRPFKATLTADTSASTAYVELSLRSEDATVYFCTRSLN 120
Db      61  GCGLEWIGNINPNSGGTNNEXFKSKATWTRDTSTSTAYWELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
```

```
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTPCPCP----- 247
      |||||
Db      239  HTPCPCPAPELAGAPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||
Qy      248  -----GQP 250
      |||||
Db      299  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
      |||||
Qy      251  REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 310
      |||||
Db      359  REPQVYTLPPSRDELTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGS 418
      |||||
Qy      311  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 354
      |||||
Db      419  FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSLSPGK 462
      |||||

RESULT 12
US-11-177-648-27
; Sequence 27, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H6
US-11-177-648-27
```

```
Query Match      86.3%; Score 1619; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 2.2e-96;
Matches 318; Conservative 11; Mismatches 23; Indels 112; Gaps 2;

Qy      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWHYKQP 60
Db      1  MGWSLILLFLVATATGVHSGVQLVQSGAEVVKPGASVKISKASGYTFTSYNWHWYRQP 60
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      61  GORLEWIGYFSPGNDDFKYNRPFKATLTADTSASTAYVELSLRSEDATVYFCTRSLN 120
Db      61  GCGLEWIGNINPNSGGTNNEXFKSKATWTRDTSTSTAYWELSSLRSEDATVYC--ELG 118
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      121  MAYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 180
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      119  QGYWGGTLLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSMNSGAL 178
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      181  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 240
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Db      179  TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKT 238
      |||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:| ||||:|
Qy      241  HTPCPCP----- 247
      |||||
Db      239  HTPCPCPAPELAGAPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
      |||||
```

```
QY 248 -----GQP 250
Db 299 VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 310
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 418
QY 311 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 354
Db 419 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 462

RESULT 13
US-11-177-648-28
; Sequence 28, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H700
US-11-177-648-28

Query Match 86.1%; Score 1616; DB 7; Length 462;
Best Local Similarity 68.5%; Pred. No. 3.3e-96;
Matches 318; Conservative 10; Mismatches 24; Indels 112; Gaps 2;

QY 1 MCWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISKASGTYFTDTHAIHWKQP 60
Db 1 MCWSCIIILFLVATATGVHSGVQLVQSGAEVVKPGASVKISKASGTYFTSYMHVWRQP 60
QY 61 GORLEWIGVSPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
Db 61 GGGLEWIGNINPNSGGTNYNEKFKSRVTMTDTSASTAYVELSLRSEDYAVYFCTRSLN 118
QY 121 MAYWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSNNGAL 180
Db 119 QGYWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSNNGAL 178
QY 181 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240
Db 179 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 238
QY 241 HTCCPPCP----- 247
Db 239 HTCCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY 248 -----GQP 250
Db 299 VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 310
```

```
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 418
QY 311 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 354
Db 419 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 462

RESULT 14
US-11-177-648-98
; Sequence 98, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H25
US-11-177-648-98

Query Match 86.0%; Score 1614; DB 7; Length 462;
Best Local Similarity 68.1%; Pred. No. 4.5e-96;
Matches 316; Conservative 12; Mismatches 24; Indels 112; Gaps 2;

QY 1 MCWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISKASGTYFTDTHAIHWKQP 60
Db 1 MCWSCIIILFLVATATGVHSGVQLVQSGAEVVKPGASVKISKASGTYFTSYMHVWRQP 60
QY 61 GORLEWIGVSPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
Db 61 GGGLEWIGNINPNSGGTNYNEKFKSRVTMTDTSASTAYVELSLRSEDYAVYFCTRSLN 118
QY 121 MAYWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSNNGAL 180
Db 119 QGYWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSNNGAL 178
QY 181 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 240
Db 179 TSGVHTFPFVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKT 238
QY 241 HTCCPPCP----- 247
Db 239 HTCCPPCPAPELAGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 298
QY 248 -----GQP 250
Db 299 VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 358
QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 310
Db 359 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGS 418
QY 311 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 354
Db 419 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 462
```

## RESULT 15

```

US-11-177-648-26
; Sequence 26, Application US/11177648
; Publication No. US2006029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 462
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H5
US-11-177-648-26

Query Match      85.9%; Score 1612; DB 7; Length 462;
Best Local Similarity 68.1%; Pred. No. 6e-96;
Matches 316; Conservative 12; Mismatches 24; Indels 112; Gaps 2;

QY   1  MGWSLIILLFVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQP  60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   1  MGWSCIIILFLVATATGVHSQVLVQSGAEVKKPGASVKSKASYGTFTSWWHVQAP  60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   61  QRLWTGYSPGNDFPKYNERFKGKATLTADTSASTAYVELSLRSEDTAVPCTRSLN  120
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   61  GGQLEWMGNINPSNGGTNYNEKFKSRVTMTDTSTSTAYMELSLRSEDTAIVYYC--ELG  118
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   121  MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGTAAALCLVCKVDYPPETPVSMNSGAL  180
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   119  QGYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGTAAALCLVCKVDYPPETPVSMNSGAL  178
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   181  TSGVHTTPAVLQSSGLYSLSVWTVTPSSSLGTQTYYICNVNHKPSNTKYDKKVEPKSCDKT  240
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   179  TSGVHTTPAVLQSSGLYSLSVWTVTPSSSLGTQTYYICNVNHKPSNTKYDKKVEPKSCDKT  238
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   241  HTCPCPCP----- 247
DB   239  HTCCPCCPAPELAGAPSVLFPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVE  298
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY   248  ----- 248
DB   299  VHNAKTKPREEQYNSTRVRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAQGQP  358
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   251  REPQVYTLPSPRDRLTNQVSRLTCLLVKGFYPDSIAVENESNGQPNENYKTTPPVLDSGGS  310
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   359  REPQVYTLPSPRDRLTNQVSRLTCLLVKGFYPDSIAVENESNGQPNENYKTTPPVLDSGGS  418
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY   311  FFLYSKULTVDKSRVOQQNVFCSVMHEALHNNHYTKSLSLSPGK  354
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB   419  FFLYSKULTVDKSRVOQQNVFCSVMHEALHNNHYTKSLSLSPGK  462
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 16, 2006, 10:38:47 ; Search time 136.475 Seconds  
(without alignments)  
1083.802 Million cell updates/sec  
Title: US-10-058-069-7  
Perfect score: 1876  
Sequence: 1 MGWSILLFLVAVATRVLSQ.....MHEALHNHYTKLSLSLSPGK 354  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main: \*  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep: \*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep: \*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep: \*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep: \*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep: \*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1770	94.3	347	5	US-10-880-028-18
2	1770	94.3	347	5	US-10-880-320-18
3	1763.5	94.0	360	5	US-10-880-028-22
4	1763.5	94.0	360	5	US-10-880-320-22
5	1762.5	93.9	362	5	US-10-880-028-23
6	1762.5	93.9	362	5	US-10-880-320-23
7	1755.5	93.6	362	5	US-10-880-028-26
8	1755.5	93.6	362	5	US-10-880-320-26
9	1613.5	86.0	731	3	US-09-825-012-45
10	1613.5	86.0	741	3	US-09-825-012-55
11	1613	86.0	470	6	US-11-019-180-4
12	1608.5	85.7	729	3	US-09-825-012-52
13	1608.5	85.7	739	3	US-09-825-012-61
14	1603	85.4	470	4	US-10-216-484-89
15	1603	85.4	470	4	US-10-384-933-89
16	1602.5	85.4	730	3	US-09-825-012-49
17	1602.5	85.4	740	3	US-09-825-012-58
18	1595	85.0	470	4	US-10-216-484-143
19	1595	85.0	470	4	US-10-384-933-143
20	1593	84.9	470	4	US-10-216-484-145
21	1593	84.9	470	4	US-10-384-933-145
22	1592	84.9	470	4	US-10-216-484-117
23	1592	84.9	470	4	US-10-216-484-147
24	1592	84.9	470	4	US-10-384-933-117
25	1592	84.9	470	4	US-10-384-933-147
26	1579	84.2	468	5	US-10-981-738-13
27	1579	84.2	470	4	US-10-216-484-157

28	1579	84.2	470	4	US-10-384-933-157	Sequence 157, App
29	1577.5	84.1	465	6	US-11-034-655-5	Sequence 5, Appl
30	1577.5	84.1	465	6	US-11-034-655-12	Sequence 12, Appl
31	1574	83.9	470	5	US-10-723-003-40	Sequence 40, Appl
32	1574	83.9	470	6	US-11-004-639-40	Sequence 40, Appl
33	1574	83.9	626	5	US-10-723-003-44	Sequence 44, Appl
34	1574	83.9	626	6	US-11-004-639-44	Sequence 44, Appl
35	1574	83.9	641	5	US-10-723-003-46	Sequence 46, Appl
36	1574	83.9	641	6	US-11-004-639-46	Sequence 46, Appl
37	1570.5	83.7	365	5	US-10-880-028-44	Sequence 44, Appl
38	1570.5	83.7	365	5	US-10-880-320-44	Sequence 44, Appl
39	1569.5	83.7	368	5	US-10-880-028-47	Sequence 47, Appl
40	1569.5	83.7	368	5	US-10-880-320-47	Sequence 47, Appl
41	1565.5	83.4	467	4	US-10-171-452A-41	Sequence 41, Appl
42	1565.5	83.4	467	4	US-10-171-452A-47	Sequence 47, Appl
43	1565.5	83.4	467	4	US-10-171-452A-53	Sequence 53, Appl
44	1565.5	83.4	467	4	US-10-171-452A-59	Sequence 59, Appl
45	1565.5	83.4	467	4	US-10-353-708-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1  
US-10-880-028-18  
; Sequence 18, Application US/10880028  
; Publication No. US20050163782A1  
; GENERAL INFORMATION:  
; APPLICANT: BRASLAWSKY, Gary R.  
; APPLICANT: GLASER, Scott  
; APPLICANT: YANG, Tzung-Hong  
; APPLICANT: HOPP, Jennifer  
; APPLICANT: CHINN, Paul  
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
; TITLE OF INVENTION: OF BINDING POLYPEPTIDES  
; FILE REFERENCE: IDV-001  
; CURRENT APPLICATION NUMBER: US/10/880,028  
; CURRENT FILING DATE: 2004-06-28  
; PRIOR APPLICATION NUMBER: 60/483877  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/508810  
; PRIOR FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: 60/515351  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: 60/516030  
; PRIOR FILING DATE: 2003-10-30  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-880-028-18

Query Match	94.3%	Score 1770;	DB 5;	Length 347;
Best Local Similarity	96.5%	Pred. No. 1.7e-112;		
Matches 335;	Conservative 0;	Mismatches 0;	Indels 12;	Gaps 1;
QY	20	QVQLVQSGAEVVPKASVKISKASGYTFTDTHAIHWKONPGORLEWIGYFSPGNDFFKY	79	
Db	1	QVQLVQSGAEVVPKASVKISKASGYTFTDTHAIHWKONPGORLEWIGYFSPGNDFFKY	60	
QY	80	NERFPGKATLTADTASTAYVELSLRSEDVAVFCTRLSNWAYWGQGLVTVSSASTKG	139	
Db	61	NERFPGKATLTADTASTAYVELSLRSEDVAVFCTRLSNWAYWGQGLVTVSSASTKG	120	
QY	140	PSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSSGLYS	199	
Db	121	PSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQSSGLYS	180	
QY	200	SSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCP	247	



;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT APPLICATION NUMBER: US/10/880,320  
;/ CURRENT FILING DATE: 2004-06-28  
;/ PRIOR APPLICATION NUMBER: 60/483877  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/508810  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR APPLICATION NUMBER: 60/515351  
;/ PRIOR FILING DATE: 2003-10-28  
;/ PRIOR APPLICATION NUMBER: 60/516030  
;/ PRIOR FILING DATE: 2003-10-30  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 22  
;/ LENGTH: 360  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Synthetic construct  
US-10-880-320-22

Query Match 94.0%; Score 1763.5; DB 5; Length 360;  
Best Local Similarity 93.1%; Pred. No. 4.9e-112;  
Matches 335; Conservative 0; Mismatches 0; Indels 25; Gaps 1;  
  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWVKONPGQRLWIGYFSPGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWVKONPGQRLWIGYFSPGNDDFKY 60  
  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSINMAYWQGGTLVTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSINMAYWQGGTLVTVSSASTKG 120  
  
QY 140 PSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 180  
  
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCP----- 247  
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPKSCDTPPPCP 240  
  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 RCPGSGSGGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300  
  
QY 295 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 5  
US-10-880-028-23  
;/ Sequence 23, Application US/10880028  
;/ Publication No. US20050163782A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: BRASLAWSKY, Gary R.  
;/ APPLICANT: GLASER, Scott  
;/ APPLICANT: YANG, Tzung-Hong  
;/ APPLICANT: HOPP, Jennifer  
;/ APPLICANT: CHINN, Paul  
;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT APPLICATION NUMBER: US/10/880,028  
;/ CURRENT FILING DATE: 2004-06-28  
;/ PRIOR APPLICATION NUMBER: 60/483877  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/508810  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR APPLICATION NUMBER: 60/515351  
;/ PRIOR FILING DATE: 2003-10-28

;/ PRIOR APPLICATION NUMBER: 60/516030  
;/ PRIOR FILING DATE: 2003-10-30  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 23  
;/ LENGTH: 362  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Synthetic construct  
US-10-880-028-23

Query Match 93.9%; Score 1762.5; DB 5; Length 362;  
Best Local Similarity 92.5%; Pred. No. 5.8e-112;  
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
  
QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWVKONPGQRLWIGYFSPGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWVKONPGQRLWIGYFSPGNDDFKY 60  
  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSINMAYWQGGTLVTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSINMAYWQGGTLVTVSSASTKG 120  
  
QY 140 PSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSL 180  
  
QY 200 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCP----- 247  
DB 181 SSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPKSCDTPPPCP 240  
  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
DB 241 RCPAPGGSGGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
  
QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 352  
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 360  
  
QY 353 GK 354  
DB 361 GK 362

RESULT 6  
US-10-880-320-23  
;/ Sequence 23, Application US/10880320  
;/ Publication No. US20050163783A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: BRASLAWSKY, Gary R.  
;/ APPLICANT: GLASER, Scott  
;/ APPLICANT: YANG, Tzung-Hong  
;/ APPLICANT: HOPP, Jennifer  
;/ APPLICANT: CHINN, Paul  
;/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS  
;/ FILE REFERENCE: IDV-001  
;/ CURRENT APPLICATION NUMBER: US/10/880,320  
;/ CURRENT FILING DATE: 2004-06-28  
;/ PRIOR APPLICATION NUMBER: 60/483877  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/508810  
;/ PRIOR FILING DATE: 2003-10-03  
;/ PRIOR APPLICATION NUMBER: 60/515351  
;/ PRIOR FILING DATE: 2003-10-28  
;/ PRIOR APPLICATION NUMBER: 60/516030  
;/ PRIOR FILING DATE: 2003-10-30  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 23  
;/ LENGTH: 362  
;/ TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-23

Query Match          93.9%; Score 1762.5; DB 5; Length 362;
Best Local Similarity 92.5%; Pred. No. 5.8e-112;
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGSGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362

RESULT 7
US-10-880-028-26
; Sequence 26, Application US/10880028
; Publication No. US20050163782A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,028
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-028-26

Query Match          93.6%; Score 1755.5; DB 5; Length 362;
Best Local Similarity 92.0%; Pred. No. 1.7e-111;
Matches 333; Conservative 1; Mismatches 1; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGSGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362

RESULT 8
US-10-880-320-26
; Sequence 26, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-26

Query Match          93.6%; Score 1755.5; DB 5; Length 362;
Best Local Similarity 92.0%; Pred. No. 1.7e-111;
Matches 333; Conservative 1; Mismatches 1; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 79
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVWKQNPQRLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 139
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSSASTKG 120

QY 140 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 199
DB 121 PSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL 180

QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 247
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCP----- 240

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292
DB 241 RCPAPGSGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300

QY 293 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 352
DB 301 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSP 360

QY 353 GK 354
DB 361 GK 362
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Db 61 NERFKGKATITADTSASTAYVELSSLRSEDATVIFCARSLNWAYMGQGLTVTVSSASTKG 120  
Qy 140 PSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 199  
Db 121 PSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 180  
Qy 200 SSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCP 247  
Db 181 SSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPKSCDTTPPCP 240  
Qy 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
Db 241 RCPAPGGSGGGSGGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
Qy 293 QPENNYKTTTPPVLDSGGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 352  
Db 301 QPENNYKTTTPPVLDSGGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 360  
Qy 353 GK 354  
Db 361 GK 362

## RESULT 9

US-09-825-012-46  
; Sequence 46, Application US/09825012  
; Patent No. US2002012798A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion  
US-09-825-012-46

Query Match 86.0%; Score 1613.5; DB 3; Length 731;  
Best Local Similarity 67.7%; Pred. No. 1.8e-101;  
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;  
Qy 1 MGSLLILFLVAVATRVLSQVOLVSGAEVVKPGASVKISCKASGYTFTDHAHWKQNP 60  
Db 1 MGWSCIILFLVATATGVHSQVOLVSGAEVVKPGASVKISCKASGYTFTDHAHWKQNP 60  
Qy 61 GORLEWIGYFSPGNDDFKYNRPFKGNATLTDTSASTAYVELSSLRSEDATVYFCTRS LN 120  
Db 61 GKGLEWVGILPGSNNSRNYEKFGKRVTVTRDTSTNTAYMELSSLRSEDATVYCARSD 120  
Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNS 177  
Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNS 180  
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 237  
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 240  
Qy 238 DKTHTCPPCP 247  
Db 241 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300  
Qy 248 ----- 247  
Db 301 GVEVHNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 360  
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 307  
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 420  
Qy 238 DKTHTCPPCP 247  
Db 241 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300  
Qy 248 ----- 247  
Db 301 GVEVHNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 360  
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 307  
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 420  
Qy 238 DKTHTCPPCP 247  
Db 241 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300  
Qy 248 ----- 247

Db 301 GVEVHNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 360  
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 307  
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 420  
Qy 308 DGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 354  
Db 421 DGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 467  
RESULT 10  
US-09-825-012-55  
; Sequence 55, Application US/09825012  
; Patent No. US2002012798A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 741  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion  
US-09-825-012-55

Query Match 86.0%; Score 1613.5; DB 3; Length 741;  
Best Local Similarity 67.7%; Pred. No. 1.8e-101;  
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;  
Qy 1 MGSLLILFLVAVATRVLSQVOLVSGAEVVKPGASVKISCKASGYTFTDHAHWKQNP 60  
Db 1 MGWSCIILFLVATATGVHSQVOLVSGAEVVKPGASVKISCKASGYTFTDHAHWKQNP 60  
Qy 61 GORLEWIGYFSPGNDDFKYNRPFKGNATLTDTSASTAYVELSSLRSEDATVYFCTRS LN 120  
Db 61 GKGLEWVGILPGSNNSRNYEKFGKRVTVTRDTSTNTAYMELSSLRSEDATVYCARSD 120  
Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNS 177  
Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNS 180  
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 237  
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC 240  
Qy 238 DKTHTCPPCP 247  
Db 241 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYD 300  
Qy 248 ----- 247  
Db 301 GVEVHNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAK 360  
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 307  
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPPVLDS 420  
Qy 308 DGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 354  
Db 421 DGSFFLYSLKLVDSRWQOGNVFSCSVNHEALHNHYTKQSLSLSP 467

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RESULT 11
US-11-019-180-4
; Sequence 4, Application US/11019180
; Publication No. US20050158828A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/11/019,180
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US/09/238,741
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-11-019-180-4

Query Match      86.0%; Score 1613; DB 6; Length 470;
Best Local Similarity 67.7%; Pred. No. 1.2e-101;
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

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Db      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVRPGASVKISKASGVTFTSYNHWKQTP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GORLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121  MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 174
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  YGDMWYFNVWGAGTTVTVSSAASKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      175  WNSGALTSQVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  WNSGALTSQVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240
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QY      235  KSCDKHTCCPPCP----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  KSCDKHTCCPPCPAPPELLGGPSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNW 300
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QY      248  ----- 247
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Db      301  YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  ----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 304
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361  KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      305  LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 354
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Db      421  LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 470
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RESULT 12
US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
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; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

Query Match      85.7%; Score 1608.5; DB 3; Length 729;
Best Local Similarity 67.6%; Pred. No. 3.9e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

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Db      1  MGWSLILLFLVAVATRVLSQVQLVQSGAEVVRPGASVKISKASGVTFTSYNHWKQNP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61  GORLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GRGLEWIGVSPGNDDFKYNRFKGGKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121  ---MAYWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVS 177
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  FAWFAYWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVS 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      178  GALTSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC 237
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  GALTSGVHTFPFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      238  DKXHTCCPPCP----- 247
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Db      241  DKXHTCCPPCPAPPELLGGPSVFLFPPPKDPTLMISRPEVTCVVVDVSHEDPEVKFNWYVD 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  ----- 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      248  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 307
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 420
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      308  DGSFELYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPG 353
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      421  DGSFELYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPG 466
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RESULT 13
US-09-825-012-61
; Sequence 61, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHHKPSNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHHKPSNTKVDKKVEP 240
Qy 235 KSCDKHTCPCP----- 247
Db 241 KSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREEQNSTYRVSVLTVLHQQWLNGKEYCKVSNKALPAPIEKTIS 360
Qy 248 ---GOPREPQVYTLPEPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
Db 361 KAKGQPREPQVYTLPEPRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Qy 305 LDSGGSFFLYSKLTVDKSRWQQGNVFPSCSMHEALHNNHYTKSLSLSPGK 354
Db 421 LDSGGSFFLYSKLTVDKSRWQQGNVFPSCSMHEALHNNHYTKSLSLSPGK 470
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Search completed: February 16, 2006, 10:43:10  
Job time : 138.475 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 10:23:17 ; Search time 39.3333 Seconds  
(without alignments)  
744.081 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSLFLFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPK 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*

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4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1559	83.1	466	2	US-09-698-705-11
3	1549	82.6	472	2	US-09-301-593-43
4	1541	82.1	449	1	US-08-458-516-13
5	1524	81.2	472	2	US-09-301-593-30
6	1509.5	80.5	489	2	US-10-104-047-3329
7	1506	80.3	476	1	US-08-378-939-10
8	1501	80.0	468	2	US-09-485-737B-67
9	1501	80.0	468	2	US-10-071-485-67
10	1501	80.0	711	2	US-09-485-737B-90
11	1495.5	79.7	467	2	US-10-071-485-90
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25	1480.5	78.9	454	1	US-07-934-373C-22
26	1480.5	78.9	454	2	US-08-437-642B-22
27	1480.5	78.9	454	2	US-08-146-206C-22

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29	1480.5	78.9	454	2	US-09-705-392A-22	Sequence 22, Appl
30	1480.5	78.9	454	2	US-09-705-398-22	Sequence 22, Appl
31	1480.5	78.9	454	4	PCT-US93-07832-22	Sequence 22, Appl
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33	1462	77.9	451	2	US-09-466-635-3	Sequence 3, Appl
34	1459.5	77.8	467	2	US-08-030-175-41	Sequence 41, Appl
35	1455.5	77.6	467	2	US-08-030-175-42	Sequence 42, Appl
36	1444	77.0	470	2	US-09-859-053-28	Sequence 28, Appl
37	1440.5	76.8	449	2	US-09-679-397-2	Sequence 2, Appl
38	1440.5	76.8	449	2	US-09-680-148-2	Sequence 2, Appl
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40	1440.5	76.8	449	2	US-10-356-974-2	Sequence 2, Appl
41	1436.5	76.3	467	1	US-07-916-098A-45	Sequence 45, Appl
42	1431.5	76.3	475	2	US-09-740-002-25	Sequence 25, Appl
43	1430	76.2	474	2	US-09-848-832-3	Sequence 3, Appl
44	1425.5	76.0	475	2	US-09-740-002-27	Sequence 27, Appl
45	1419	75.6	470	2	US-10-104-047-3730	Sequence 3730, Ap

ALIGNMENTS

RESULT 1

US-09-238-741-4

; Sequence 4, Application US/09238741

; Patent No. 6897044

; GENERAL INFORMATION:

; APPLICANT: BRASLAWSKY, GARY R.

; APPLICANT: HANNA, NABIL

; APPLICANT: HARIHARAN, KANDASAMY

; APPLICANT: LABARRE, MICHAEL J.

; APPLICANT: HUYNH, TRI B.

; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES

; FILE REFERENCE: 23522.0584

; CURRENT APPLICATION NUMBER: US/09/238,741

; CURRENT FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)

US-09-238-741-4

Query Match	86.0%	Score 1613;	DB 2;	Length 470;
Best Local Similarity	67.7%;	Pred. No. 1.3e-115;		
Matches 318;	Conservative 13;	Mismatches 23;	Indels 116;	Gaps 2;
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DB	1	MGWSLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTSYNNHWKQTP	60	
QY	61	GORLEWIGVFSQNDDFKYNRERFKGKATLTADTASTAYVELSSLRSEDTAVYFCTRSLN	120	
DB	61	GRGLEWIGAIYFGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYVCARSTY	120	
QY	121	MA-----VWGQGLTVTVSSASTKGFSPFLAPSSKSTSGGTAALGCLVKDYPPPEPTVVS	174	
DB	121	YGGDWYFNWVGAGTTVTVSAASTKGFSPFLAPSSKSTSGGTAALGCLVKDYPPPEPTVVS	180	
QY	175	WNSGALTSGVHTFPVAVLQSSGLYSLSVVTVFSSSLGTOTYICNVNHNKPSNTKVDKKVSP	234	
DB	181	WNSGALTSGVHTFPVAVLQSSGLYSLSVVTVFSSSLGTOTYICNVNHNKPSNTKVDKKVSP	240	
QY	235	KSCDKTHTCPPCP-----	247	
DB	241	KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNW	300	
QY	248	-----	247	

Db 301 YVDGVEVNAKTPREBQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304

Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420

Qy 305 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

Db 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 2

US-09-698-705-11

Sequence 11, Application US/09698705

Patent No. 6824780

GENERAL INFORMATION:

APPLICANT: Devaux, B.

APPLICANT: Keller, G.

APPLICANT: Koepfen, H.

APPLICANT: Lasky, L.

TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

FILE REFERENCE: P177R1

CURRENT APPLICATION NUMBER: US/09/698,705

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/182,872

PRIOR FILING DATE: 2000-02-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 11

LENGTH: 466

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: sequence is chimeric mouse/human

US-09-698-705-11

Query Match 83.1%; Score 1559; DB 2; Length 466;

Best Local Similarity 65.5%; Pred. No. 1.8e-111;

Matches 305; Conservative 21; Mismatches 28; Indels 112; Gaps 2;

Qy 1 MCWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60

Db 1 MCWSLILLFLVATATGVHSQVQVQPGAEIVAPGVKLSCKASGYTFNYMLNWKQRP 60

Qy 61 GQRLWIGVYFSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSSEDTAVYFC--TRS 118

Db 61 GRGLEWIGRIDPSDSEIHYDQFKDKATLTVDKSSSTAYIQLSSLTSEDSAVVYCALTGI 120

Qy 119 LNAVYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG 178

Db 121 YAMAYWGQGSTVTVSSAKTTPGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG 180

Qy 179 ALTSGVHTFPVAVLQSSGLYSLSVTVPPSSSLGTQYICNVNHPKSNKTKVDKVPKSCD 238

Db 181 ALTSGVHTFPVAVLQSSGLYSLSVTVPPSSSLGTQYICNVNHPKSNKTKVDKVPKSCD 240

Qy 239 KHTCTPPCP----- 247

Db 241 KHTCTPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 300

Qy 248 -----G 248

Db 301 VEVHNAKTPREBQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAG 360

Qy 249 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 308

Db 361 QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD 420

Qy 309 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

Db 421 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 466

RESULT 3

US-09-301-593-43

Sequence 43, Application US/09301593A

Patent No. 6455677

GENERAL INFORMATION:

APPLICANT: Park, John B.

APPLICANT: Garin-Chesa, Pilar

APPLICANT: Bamberger, Uwe

APPLICANT: Leger, Olivier

APPLICANT: Saldanha, Jose W.

APPLICANT: Rettig, Wolfgang J.

TITLE OF INVENTION: EAP-specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A

CURRENT FILING DATE: 1999-04-29

EARLIER APPLICATION NUMBER: EP 98107925.4

EARLIER FILING DATE: 1998-04-30

EARLIER APPLICATION NUMBER: US 60/086,049

EARLIER FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 43

LENGTH: 472

TYPE: PRT

ORGANISM: Homo sapiens

US-09-301-593-43

Query Match 82.6%; Score 1549; DB 2; Length 472;

Best Local Similarity 65.3%; Pred. No. 1e-110;

Matches 309; Conservative 15; Mismatches 29; Indels 120; Gaps 3;

Qy 1 MCWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60

Db 1 MDWTWRVFCLLAVAPGAHSQVLQVSGAEVVKPGASVKISCKASGYTFEYTIHWVQAP 60

Qy 61 GQRLWIGVYFSPGNDDFKYNRFKGGKATLTADTSASTAYVELSSLRSSEDTAVYFC-- 117

Db 61 GQRLWIGVGINPNNIGIPNYNQKFGKRALTVGKSASTAYMELSSLRSSEDTAVYFCARRI 120

Qy 118 -----SLNMAVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV 171

Db 121 AVGYDEGHANDYWGQGLTVTVSS--STKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPV 179

Qy 172 TVSNWSGALTSGVHTFPVAVLQSSGLYSLSVTVPPSSSLGTQYICNVNHPKSNKTKVDK 231

Db 180 TVSNWSGALTSGVHTFPVAVLQSSGLYSLSVTVPPSSSLGTQYICNVNHPKSNKTKVDK 239

Qy 232 VEPKSCDKTHTCPPCP----- 247

Db 240 VEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVK 299

Qy 248 ----- 247

Db 300 FNNVYDGVVEVHNAKTPREBQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEK 359

Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 301

Db 360 TISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 419

Qy 302 PVPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

Db 420 PVPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 4

US-08-458-516-13

Sequence 13, Application US/08458516

Patent No. 5777085

GENERAL INFORMATION:

APPLICANT: Co, Man Sung

APPLICANT: Tso, J. Yun

/ TITLE OF INVENTION: Humanized Antibodies Reactive with  
/ TITLE OF INVENTION: GPIIB/IIIA  
/ NUMBER OF SEQUENCES: 23  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: William M. Smith  
/ STREET: One Market Plaza, Steuart Tower, Suite 2000  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94105  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/458,516  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/059,159  
/ FILING DATE: 03-MAY-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Smith, William M.  
/ REGISTRATION NUMBER: 30,223  
/ REFERENCE/DOCKET NUMBER: 11823-37-3  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-326-2400  
/ TELEFAX: 415-326-2422  
/ INFORMATION FOR SEQ ID NO: 13:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 449 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-08-458-516-13

Query Match 82.1%; Score 1541; DB 1; Length 449;  
Best Local Similarity 67.5%; Pred. No. 4e-110;  
Matches 303; Conservative 10; Mismatches 22; Indels 114; Gaps 2;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPGRLEWIGYFSGNDDFKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPGRLEWIGYFSGNDDFKY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTRSLN----MAYGQGTLTVTSSA 135  
DB 61 NEKFKGRVLTVDSTNTAYMELSLRSEDATVYFCARRDGNVGFAYWGQGTLTVTSSA 120  
QY 136 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSSG 195  
DB 121 SYKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSSG 180  
QY 196 LYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKKEPKSCDKTHHTCPCP----- 247  
DB 181 LYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKKEPKSCDKTHHTCPCPAPPELLGGP 240  
QY 248 ----- 247  
DB 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNPNVVDGVEVHNAKTKPREEQYNS 300  
QY 248 -----GQPREPQVYTLPPSRDEL 265  
DB 301 TYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360  
QY 266 TRNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 325  
DB 361 TRNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 420  
QY 326 QGNVFSCSVHNEALHNHYTQKSLSLSPGK 354  
DB 421 QGNVFSCSVHNEALHNHYTQKSLSLSPGK 449

## RESULT 5

US-09-301-593-30  
/ Sequence 30, Application US/09301593A  
/ Patent No. 6455677  
/ GENERAL INFORMATION:  
/ APPLICANT: Park, John E.  
/ APPLICANT: Garin-Chesa, Pilar  
/ APPLICANT: Bamberger, Uwe  
/ APPLICANT: Leger, Olivier  
/ APPLICANT: Saldanha, Jose W.  
/ APPLICANT: Rettig, Wolfgang J.  
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
/ FILE REFERENCE: 0652.1890001  
/ CURRENT APPLICATION NUMBER: US/09/301,593A  
/ CURRENT FILING DATE: 1999-04-29  
/ EARLIER APPLICATION NUMBER: EP 98107925.4  
/ EARLIER FILING DATE: 1998-04-30  
/ EARLIER APPLICATION NUMBER: US 60/086,049  
/ EARLIER FILING DATE: 1998-05-18  
/ NUMBER OF SEQ ID NOS: 108  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 30  
/ LENGTH: 472  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ US-09-301-593-30

Query Match 81.2%; Score 1524; DB 2; Length 472;  
Best Local Similarity 63.8%; Pred. No. 8.5e-109;  
Matches 302; Conservative 20; Mismatches 31; Indels 120; Gaps 3;  
QY 1 MGMSLLFLVAVATRVLSQVLQVSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60  
DB 1 MGMSWVFLFLSGTAGVLSQVQLQSGPELVKPGASVKISKASGYTFDTHAIHWKQNP 60  
QY 61 GORLEWIGYFSGNDDFKYNERFKGKATLTADTSASTAYVELSLRSEDATVYFCTR--- 117  
DB 61 GKSLEWIGGINPNNGIPNYPNQFKGRATLTVGKSSSTAYMELSLRSEDATVYFCARRRI 120  
QY 118 -----SLNMAWYGQGTLTVTSSASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPV 171  
DB 121 AVYDEGHAMDYWGQGTSTVTVSS-STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPV 179  
QY 172 TVSWNSGALTSGVHTTTPAVLQSSGLYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKK 231  
DB 180 TVSWNSGALTSGVHTTTPAVLQSSGLYSLSVSVTVTPSSSLGTQTYICNVNHPKNTKVDKK 239  
QY 232 VEPKSCDKTHHTCPCP----- 247  
DB 240 VEPKSCDKTHHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 299  
QY 248 ----- 247  
DB 300 FNNYVDGVEVHNAKTKPREEQYNSTYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEK 359  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 301  
DB 360 TTSKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 419  
QY 302 PPLVSDSGSFFLYSKLTVDKSRWQQGNVFPSCSVHNEALHNHYTQKSLSLSPGK 354  
DB 420 PPLVSDSGSFFLYSKLTVDKSRWQQGNVFPSCSVHNEALHNHYTQKSLSLSPGK 472

## RESULT 6

US-10-104-047-3329  
/ Sequence 3329, Application US/10104047  
/ Patent No. 6943241  
/ GENERAL INFORMATION:  
/ APPLICANT: HELIX RESEARCH INSTITUTE  
/ TITLE OF INVENTION: No. 6943241el full length cdna

```
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3329
; LENGTH: 489
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-104-047-3329

Query Match      80.5%; Score 1509.5; DB 2; Length 489;
Best Local Similarity 60.9%; Pred. No. 1.1e-107;
Matches 298; Conservative 21; Mismatches 35; Indels 135; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MDWTRVFCLLAVAPGAHSQVQLVQSGAEVVKPGASVRVSCAFGFTFTYQIHWRQAP 60
QY 61 GQRLWIGYFSPGNDDFKYNRPFKATLTADTSAAYVELSLRSEDYAVYFCTR--- 117
Db 61 GQGLEWVGVSFPGGSATYAQRFGQRTVITRDTSTSTVTMDLSLRSDDSAVYCARVVS 120
QY 118 -----SLNWAYWGQGLTLTVSSASTKGPSVFPPLAPSSKSTSGG 155
Db 121 ELFSFGGGTLTLDRIKVPNNHYSYGMVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGG 180
QY 156 TAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTY 215
Db 181 TAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTY 240
QY 216 ICNVNHPKSNKTKVDKVEPKSCDKHTCTCPPCP----- 247
Db 241 ICNVNHPKSNKTKVDKVEPKSCDKHTCTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPE 300
QY 248 ----- 247
Db 301 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE 360
QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA 285
Db 361 YKCKVSNKALPAPIEKTIISKAGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA 420
QY 286 VEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ 345
Db 421 VEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQ 480
QY 346 KSLSLSPGK 354
Db 481 KSLSLSPGK 489

RESULT 7
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: LEWIS, ALAN PETER
; APPLICANT: CROWE, JAMES SCOTT
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSES: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-10

Query Match      80.3%; Score 1506; DB 1; Length 476;
Best Local Similarity 63.4%; Pred. No. 2.1e-107;
Matches 302; Conservative 20; Mismatches 32; Indels 122; Gaps 3;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MDWTRFLFVVAATGVSQMQVQSGAEVVKPGSVTVSCASGSGTFSYAISWVRQAP 60
QY 61 GQRLWIGYFSPGNDDFKYNRPFKATLTADTSAAYVELSLRSEDYAVYFCT--- 116
Db 61 GQGLEWVGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDYAVYCATDRY 120
QY 117 RSLNWAY-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 168
Db 121 ROANFDRARVGVDFDPAGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 169 EPTVTVSNWNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKV 228
Db 181 EPTVTVSNWNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKV 240
QY 229 DKKVEPKSCDKHTCTCPPCP----- 247
Db 241 DKKVEPKSCDKHTCTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 248 ----- 247
Db 301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 298
Db 361 IEKTTISKAGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 299 KTTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSLSPGK 354
Db 421 KTTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSLSPGK 476

RESULT 8
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
```

Query Match 80.0%; Score 1501; DB 2; Length 468;  
Best Local Similarity 63.8%; Pred. No. 4.9e-107;  
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2;

QY	7	IPSP	LLISASVILSOVLQVSGSELKPGASVKLSCKASGYTTDYGMMVWKQAPGOGLK	66
QY	66	WIGF	SPGNDPDKYNERAFKGAATLTDASTAYVELSSLRSEDYVYFCFTRG--LN	123
Db	67	WNGH	INTYTGSTVYDDEKGRFVPSLDTSYAAVLQISSLKAEDETATYFCARRGFFAMDY	126
QY	124	MGQGT	LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSG	183
Db	127	MGQGT	LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWMNSGALTSG	186
QY	184	VHTF	PAVLQSSGLYSLSGVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTC	243
Db	187	VHTF	PAVLQSSGLYSLSGVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTC	246
QY	244	PPCP	-----	247
Db	247	PPCP	APPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV	306
QY	248	-----	-----GQPREP	253
Db	307	AKTR	PREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSKALPASIEKTISKAKGQPREP	366
QY	254	QVYTL	PPSRDLTKNQVSLTCLVKGFPSDIAVWEWSNGQPENNYKTTTPVLDSGSGFFL	313
Db	367	QVYTL	PPSRDEWTKNQVSLTCLVKGFPSDIAVWEWSNGQPENNYKTTTPVLDSGSGFFL	426
QY	314	YSKLT	VDKSRVQGGQGVFSCSYMHREALHNYHTQKSLSLSPGK	354
Db	427	YSKLT	VDKSRVQGGQGVFSCSYMHREALHNYHTQKSLSLSPGK	467

/ APPLICANT: Buyse, Marie-Ange  
 / APPLICANT: Sadlon, Erwin  
 / TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
 / TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
 / FILE REFERENCES: INNS:015  
 / CURRENT APPLICATION NUMBER: US/09/485,737B  
 / CURRENT FILING DATE: 2000-02-14  
 / PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
 / PRIOR FILING DATE: 1998-08-14  
 / PRIOR APPLICATION NUMBER: EPO 98870139.7  
 / PRIOR FILING DATE: 1998-06-18  
 / PRIOR APPLICATION NUMBER: EPO 97870122.5  
 / PRIOR FILING DATE: 1997-08-18  
 / NUMBER OF SEQ ID NOS: 104  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 90  
 / LENGTH: 711  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:

```

; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match      80.0%; Score 1501; DB 2; Length 711;
Best Local Similarity 63.8%; Pred. No. 8.2e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2

Qy 6 ILPLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNGORLE 65
Db 7 IFSELLISAVLSQVLVQSGSELKPGASVKISKASGYTFTDYGNNWVKQAPGQGLK 66
Qy 66 WIGVFSPGNDDFKNERFKGKATLTADTASATYAVVELSSLRSEDATVVPCTRS--LNW 123
Db 67 WMGHINTYTGSTVVDDEFKGRFVSLDTSVSNAYLIQISLKAEDTATYFCARRGFVAMDY 126
Qy 124 WGQGTLLVTVSSASTKGPSVFFPLAPSSKSTSGTGAALGCLVVDYFPPEPTVTVSNW 183
Db 127 WGQGTLLVTVSSASTKGPSVFFPLAPSSKSTSGTGAALGCLVVDYFPPEPTVTVSNW 186
Qy 184 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTVICNNHKNPSNTKVDKVEPKSCDKTHTC 243
Db 187 VHTPEAVLQSSGLYSLSVTVTPSSSLGTQTVICNNHKNPSNTKVDKVEPKSCDKTHTC 246
Qy 244 PPCP----- 247
Db 247 PPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 306
Qy 248 ----- 249
Db 307 AKTKPRBEQYNSTYRVWVSLTVLHODWLNKGEYKCKVSNKALPASEIKTISKAKGP 366
Qy 254 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 313
Db 367 QVYTLPPSRDEWTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 426
Qy 314 YSKLTVDKSRWQOQGVNFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 427 YSKLTVDKSRWQOQGVNFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 11
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 90
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match      80.0%; Score 1501; DB 2; Length 711;
Best Local Similarity 63.8%; Pred. No. 8.2e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGTUT1  
CLONE: 2747531  
US-09-049-672A-8

Query Match 79.7%; Score 1495.5; DB 2; Length 467;  
Best Local Similarity 63.3%; Pred. No. 1.3e-106;  
Matches 292; Conservative 26; Mismatches 30; Indels 113; Gaps 2;  
QY 7 LFLVAVATVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQGORLEW 66  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 66  
7 ILFLVAATCTHAQVLQSGAEVVKPGASVQSVCTVSGFTLSDLSVHWVRAQAGQGLEW 66  
QY 67 IGVFSGNDDFKNERPKGKATLTADTSASTAYVELSLRSEDYAVYFCTR---SLNWAY 123  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 123  
67 MGLAPENGAEVYAKFLGRLTLSEDTADTAYMFLNNLGSSEDAIYYCARQHYDFFDF 126  
QY 124 WGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSG 183  
DB 127 WGGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSG 186  
QY 184 VHTFPAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTC 243  
DB 187 VHTFPAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTC 246  
QY 244 PCPC----- 247  
DB 247 PPCPAELGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 306  
QY 248 -----GQPREP 253  
DB 307 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 366  
QY 254 QVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 313  
DB 367 QVYTLPPSDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 426  
QY 314 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 427 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 13  
US-09-301-593-18  
Sequence 18, Application US/09301593A  
Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652,1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18  
LENGTH: 453  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-18  
Query Match 79.2%; Score 1486.5; DB 2; Length 453;  
Best Local Similarity 64.7%; Pred. No. 6.1e-106;  
Matches 293; Conservative 16; Mismatches 25; Indels 119; Gaps 2;  
QY 21 VOLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQGORLEWIGYFSPGNDDFKYN 80  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60  
1 VOLQSGPELVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLWIGGINPNNGLPNYN 60  
QY 81 ERFKGAATLTADTSASTAYVELSLRSEDYAVYFCTR-----SLNWAYGQGTTLVT 131  
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120  
61 QKFKGRATLTGKSSSTAYMELRSLTSEDSAVVFCARRRIAYGYDEGHAMDYWGQTSVT 120  
QY 132 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 191  
DB 121 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180  
QY 192 QSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTTCCPCP--- 247  
DB 181 QSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVPEKSCDKHTTCCPCPAPEL 240  
QY 248 ----- 247  
DB 241 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREE 300  
QY 248 -----GQPREPQVYTLPPS 261  
DB 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 360  
QY 262 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 321  
DB 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420  
QY 322 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 14  
US-09-627-896B-24  
Sequence 24, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARRENO, BEATRIZ  
APPLICANT: CELNIKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY  
APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEERTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
FILE REFERENCE: 08702.0081-01000  
CURRENT APPLICATION NUMBER: US/09/627,896B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 462  
TYPE: PRT  
ORGANISM: 3D1 heavy chain  
US-09-627-896B-24  
Query Match 79.2%; Score 1485; DB 2; Length 462;

Best Local Similarity	63.9%;	Pred. No. 8.1e-106;	
Matches	297;	Conservative	21; Mismatches 33; Indels 114; Gaps 4;

  

QY	1	MGMSLILLFLAVATRVLSQVLQVSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP	60
		:     :     :     :     :     :     :     :     :     :     :	
Db	1	MGWNCIIPLFVLTATGVHSQVLQVSGAEVVKPGSSVKVSKASGYTFDVAIQWVQAP	60
		:     :     :     :     :     :     :     :     :     :	
QY	61	GORLEWIGYFSPGNDDFKYNREFKGAATLTDATSAAYVELSSLRSSEDTAVYFCTRSL-	119
		:     :     :     :     :     :     :     :     :     :	
Db	61	CGGLEWIGVINIYYDNTNYNQKFGKATWVDKSTSTAYMELSSLRSSEDTAVYYCARAAW	120
		:     :     :     :     :     :     :     :     :     :	
QY	120	NYAYWCGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLYKDYFPEPVTVMNSGA	179
		:     :     :     :     :     :     :     :     :     :	
Db	121	YMDYWGQGLTVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLYKDYFPEPVTVMNSGA	180
		:     :     :     :     :     :     :     :     :     :	
QY	180	LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLCTQTYICNVNHPKNT-KVDKKEPKSCD	238
		:     :     :     :     :     :     :     :     :     :	
Db	181	LTSGVHTFPAVLQSSGLYSLSSVTVPSNFTQTYICNVDPKPSNTKKVDKTVVERKCCV	240
		:     :     :     :     :     :     :     :     :     :	
QY	239	KTHTCPPCP-----	247
Db	241	E---CPPCAPPAAPAAAPSVLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV	297
QY	248	-----GQ	249
Db	298	EVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQ	357
QY	250	PREPQVYTLPPSRDELTKNQVSLTCLVKGFGYPSDIAVESWNGQPPENNYKTPPVLDSGD	309
		:     :     :     :     :     :     :     :     :     :	
Db	358	PREPQVYTLPPSRDELTKNQVSLTCLVKGFGYPSDIAVESWNGQPPENNYKTPPVLDSGD	417
		:     :     :     :     :     :     :     :     :     :	
QY	310	SPELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	354
		:     :     :     :     :     :     :     :     :     :	
Db	418	SPELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	462
		:     :     :     :     :     :     :     :     :     :	

  

RESULT 15	US-08-487-550-8
	; Sequence 8, Application US/08487550
	; Patent No. 6113898
	; GENERAL INFORMATION:
	; APPLICANT: Anderson, Darrell R.
	; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
	; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
	; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
	; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
	; NUMBER OF SEQUENCES: 12
	; CORRESPONDENCE ADDRESS:
	; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
	; STREET: 699 Prince Street
	; CITY: Alexandria
	; STATE: VA
	; COUNTRY: USA
	; ZIP: 22314
	; COMPUTER READABLE FORM:
	; MEDIUM TYPE: Floppy disk
	; COMPUTER: IBM PC compatible
	; OPERATING SYSTEM: PC-DOS/MS-DOS
	; SOFTWARE: Patentin Release #1.0, Version #1.30
	; CURRENT APPLICATION DATA:
	; APPLICATION NUMBER: US/08/487,550
	; FILING DATE: 07-JUN-1995
	; CLASSIFICATION: 435
	; ATTORNEY/AGENT INFORMATION:
	; NAME: Teskin, Robin L.
	; REGISTRATION NUMBER: 35,030
	; REFERENCE/DOCKET NUMBER: 012712-131
	; TELECOMMUNICATION INFORMATION:
	; TELEPHONE: 703-836-6620
	; TELEFAX: 703-836-2021
	; INFORMATION FOR SEQ ID NO: 8:
	; SEQUENCE CHARACTERISTICS:
	; LENGTH: 478 amino acids



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:12:11 ; Search time 182.96 Seconds  
(without alignments)  
1365.094 Million cell updates/sec

Title: US-10-058-069-7  
Perfect score: 1876  
Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1521.5	81.1	469	2 Q7Z7P5 HUMAN	Q7Z7P5 homo sapien
2	1500.5	80.0	475	2 Q6N095 HUMAN	Q6N095 homo sapien
3	1479	78.8	480	2 Q6PJF1 HUMAN	Q6PJF1 homo sapien
4	1457.5	77.7	469	2 Q569F4 HUMAN	Q569F4 homo sapien
5	1452.5	77.4	475	2 Q5EEF5 HUMAN	Q5EEF5 homo sapien
6	1440	76.8	472	2 Q6N089 HUMAN	Q6N089 homo sapien
7	1439	76.7	518	2 Q6N030 HUMAN	Q6N030 homo sapien
8	1430.5	76.3	475	2 Q6MZQ6 HUMAN	Q6MZQ6 homo sapien
9	1427.5	76.1	544	2 Q6PJ95 HUMAN	Q6PJ95 homo sapien
10	1426	76.0	466	2 Q6IN78 HUMAN	Q6IN78 homo sapien
11	1425	76.0	470	2 Q6PJ44 HUMAN	Q6PJ44 homo sapien
12	1422.5	75.8	475	2 Q6GMW7 HUMAN	Q6GMW7 homo sapien
13	1417	75.5	466	2 Q6N096 HUMAN	Q6N096 homo sapien
14	1411.5	75.2	475	2 Q5RE17 PONY	Q5RE17 pongo pygma
15	1410	75.2	478	2 Q6PI81 HUMAN	Q6PI81 homo sapien
16	1407.5	75.0	473	2 Q6MZV7 HUMAN	Q6MZV7 homo sapien
17	1402	74.7	480	2 Q6N094 HUMAN	Q6N094 homo sapien
18	1400	74.6	482	2 Q7Z351 HUMAN	Q7Z351 homo sapien
19	1398.5	74.5	473	2 Q6P055 HUMAN	Q6P055 homo sapien
20	1392	74.2	470	2 Q7Z5W1 HUMAN	Q7Z5W1 homo sapien
21	1388.5	74.0	519	2 Q5E3M2 HUMAN	Q5E3M2 homo sapien
22	1379.5	73.5	465	2 Q6GMX6 HUMAN	Q6GMX6 homo sapien
23	1377.5	73.4	481	2 Q6N097 HUMAN	Q6N097 homo sapien
24	1374	73.2	476	2 Q6GMX1 HUMAN	Q6GMX1 homo sapien
25	1330	70.9	464	2 Q6MZU6 HUMAN	Q6MZU6 homo sapien
26	1322	70.5	470	2 Q68CN4 HUMAN	Q68CN4 homo sapien
27	1285.5	68.5	465	2 Q6P6C4 HUMAN	Q6P6C4 homo sapien
28	1284.5	68.5	521	2 Q8N4Y9 HUMAN	Q8N4Y9 homo sapien
29	1219	65.0	458	2 Q5BJZ2 RAT	Q5BJZ2 rattus norv
30	1218	64.9	417	2 Q6N093 HUMAN	Q6N093 homo sapien
31	1205	64.2	473	2 Q8TC63 HUMAN	Q8TC63 homo sapien

32	1195.5	63.7	476	2 Q6MXZ7 HUMAN	Q6mxz7 homo sapien
33	1162	61.9	348	2 Q6PYX1 HUMAN	Q6pyx1 homo sapien
34	1148.5	61.2	465	2 Q6FJB2 MOUSE	Q6fjb2 mus musculus
35	1148	61.2	458	2 Q5BK05 RAT	Q5bk05 rattus norv
36	1138.5	60.7	473	2 Q9D8L4 MOUSE	Q9d8l4 mus musculus
37	1121.5	59.8	463	2 Q99LC4 MOUSE	Q99lc4 mus musculus
38	1116	59.5	330	1 IGHG1 HUMAN	P01857 homo sapien
39	1107	59.0	468	2 Q569W9 MOUSE	Q569w9 mus musculus
40	1101	58.7	470	2 Q7TMK1 MOUSE	Q7tmk1 mus musculus
41	1100	58.6	464	2 Q6PF95 MOUSE	Q6pf95 mus musculus
42	1096	58.4	472	2 Q6PJA7 MOUSE	Q6pja7 mus musculus
43	1087.5	58.0	487	2 Q6SZL2 9MURI	Q6szl2 mus sp. fv/
44	1083.5	57.8	477	2 Q58E56 MOUSE	Q58e56 mus musculus
45	1058	56.4	468	2 Q505N9 MOUSE	Q505n9 mus musculus

ALIGNMENTS

RESULT 1  
Q7Z7P5 HUMAN  
ID Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q7Z7P5;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
RN NCBI\_TaxID=9606;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splice;  
RG NIH MGC Project;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051328; AAHS1328.1; -; mRNA.  
DR HSSP; P01857; 1HZH.  
DR SMR; Q7Z7P5; 20-469.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

KW Immunoglobulin domain.  
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;  
Query Match 81.1%; Score 1521.5; DB 2; Length 469;  
Best Local Similarity 64.0%; Pred. NO. 2.9e-101;  
Matches 300; Conservative 21; Mismatches 33; Indels 115; Gaps 3;  
QY 1 MWSLLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60  
DB 1 MDWTSILFLVAATGARFQVHLVQSGAEVVKPGASVKLSCKTSGYNFSSYDLIHWVROAP 60  
QY 61 GORLEWIGVPSGNDDFKYNRFKGAATLTADTSASTAYVELSLRSEDATVFC-TRSL 119  
DB 61 GQGLEWMGHSIHANGDTKARKFQGRVTWTTDSATTSWEFRSLRSDDTALFYCATKSR 120  
QY 120 NMA-----YWGQGTFLVTVSSASTKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSW 175  
DB 121 GQVGFDSGQGTFLVTVSSASTKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSW 180  
QY 176 NSGALTSGVHTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKEVPK 235  
DB 181 NSGALTSGVHTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKEVPK 240  
QY 236 SCDKTHTCPPCP----- 247  
DB 241 SCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWY 300  
QY 248 ----- 247  
DB 301 VDGVEVHNAKTPREBQYNSYTRVSVLTVLHQDWLNGKEYCKCKSNKALPAPIETKISK 360  
QY 248 --GQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVVL 305  
DB 361 AKGQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVVL 420  
QY 306 DSDGSFLLSKLTVDKSRWQGNVFCVSMVHEALHNHYTKSLSPGK 354  
DB 421 DSDGSFLLSKLTVDKSRWQGNVFCVSMVHEALHNHYTKSLSPGK 469

RESULT 2  
Q6N095 HUMAN  
ID Q6N095\_HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6N095  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686K03196.  
GN Names=DKFZp686K03196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640621; CAE45775.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR SMR; Q6N095; 20-475.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;  
Query Match 80.0%; Score 1500.5; DB 2; Length 475;  
Best Local Similarity 62.3%; Pred. NO. 9.7e-100;  
Matches 296; Conservative 24; Mismatches 34; Indels 121; Gaps 2;  
QY 1 MWSLLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60  
DB 1 MDWTSILFLVAATGARFQVHLVQSGAEVVKPGASVKLSCKTSGYNFSSYDLIHWVROAP 60  
QY 61 GORLEWIGVPSGNDDFKYNRFKGAATLTADTSASTAYVELSLRSEDATVFC-TRSL 120  
DB 61 GORLEWIGVPSGNDDFKYNRFKGAATLTADTSASTAYVELSLRSEDATVFC-TRSL 120  
QY 121 -----MAYMGQGTFLVTVSSASTKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPE 169  
DB 121 GRALWFGELDAFDINGQGTGKTVTVSSASTKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPE 180  
QY 170 PVTVSNWNSGALTSGVHTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVD 229  
DB 181 PVTVSNWNSGALTSGVHTPPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVD 240  
QY 230 KKEVPKSCDKTHTCPPCP----- 247  
DB 241 KKEVPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPE 300  
QY 248 ----- 247  
DB 301 VKFNWYVDGVEVHNAKTPREBQYNSYTRVSVLTVLHQDWLNGKEYCKCKSNKALPAPI 360  
QY 248 -----GQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYK 299  
DB 361 ERTISKAKGQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPENNYK 420  
QY 300 TTPPVLDSDGSFLLSKLTVDKSRWQGNVFCVSMVHEALHNHYTKSLSPGK 354  
DB 421 TTPPVLDSDGSFLLSKLTVDKSRWQGNVFCVSMVHEALHNHYTKSLSPGK 475

RESULT 3  
Q6PJF1 HUMAN  
ID Q6PJF1\_HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6PJF1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McQuellano J.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX STRAUSBERG R.;
RA Submitter (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC016381; AAH16381.1; -, mRNA.
DR HSPF; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR0031006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;

Query Match 78.8%; Score 1479; DB 2; Length 480;
Best Local Similarity 61.7%; Pred. No. 3.5e-98;
Matches 296; Conservative 18; Mismatches 40; Indels 126; Gaps 2;

QY 1 MGWSLLFLVAVATVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
DB 1 MDWTRFLFVAAATGVQSQVQLVQSGAEVVKPGSSVKSKASGSGSPGFSVLSWVRQAP 60
QY 61 GQRLWIGVFGPNDDFKYNRERKPKATLTADTSASTAYVELSLRSEDYAVFCFTRL- 119
DB 61 GQGLAWMGGIAPAFDITKYAQNQDRVTISADESTDTAYMELSLRSEDYATYYCARDLA 120
QY 120 -----NNAYVGGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVK 164
DB 121 LVELNSGFTDEKYGIDLVWGQGTPTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVK 180
QY 165 DYPPEPVTWNSGALTSVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPS 224
DB 181 DYPPEPVTWNSGALTSVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPS 240
QY 225 NTKVDKVKPKSCDKTHTCPPCP----- 247
DB 241 NTKVDKRVKPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVS 300
QY 248 ----- 247
DB 301 HEDPEVKFNWYDGVVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294
DB 361 LPAPIEKTIKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 420
QY 295 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 421 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 480

RESULT 4
Q569F4_HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 77.7%; Score 1457.5; DB 2; Length 469;
Best Local Similarity 61.2%; Pred. No. 1.2e-96;
Matches 287; Conservative 29; Mismatches 38; Indels 115; Gaps 3;

QY 1 MGWSLLFLVAVATVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
DB 1 MBFGLSWVFLVAILKGVQCEVLVESGVVPGGSLRSLRSCASGTFDDIYANHWVRQAP 60
QY 61 GQRLWIGVFGPNDDFKYNRERKPKATLTADTSASTAYVELSLRSEDYAVFC-TR-- 117
DB 61 GKGLWVSLISWDGSGTYYADSVKGRFTISRDNSKNSLYLQMNSLRADTALYYCATRG 120
QY 118 --SLNAYVGGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPEPVTW 175
DB 121 YSTAGPDYVGGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPEPVTW 180
QY 176 NSGALTSVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVKPK 235
DB 181 NSGALTSVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVKPK 240
QY 236 SCDKTHTCPPCP----- 247
DB 241 SCDKTHTCPPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 VDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIK 360
QY 248 --GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 305
DB 361 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 420
QY 306 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 421 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469
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Db 421 TTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHHTQKSLSLSPGK 475

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RESULT 5
QSEFES HUMAN
ID QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DE Anti-Rnd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RT antibody T125."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 475 AA; 52362 MW; 1367D40DC7D2859 CRC64;

Query Match 77.4%; Score 1452.5; DB 2; Length 475;
Best Local Similarity 60.2%; Pred. No. 2.8e-96;
Matches 286; Conservative 27; Mismatches 41; Indels 121; Gaps 2;

QY 1 MGSLLILLFLVAVATVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MEFGLSWFLVALLRGVQCVQLVESGGGVQPGSRSLRSTASGTFKRYAMHWVRQAP 60

QY 61 GORLEWIGYFSPGNDPFKYNRFKGNATLTADTSASTAYVELSLRSEDVAVYFCTRSLN 120
DB 61 AKGLEWVAISYDGRNIQYADSVKGRCTPSRDNSTQTLVQLNSLRPEDTAVYVCARPYR 120

QY 121 MAY-----WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPE 169
DB 121 SRWLQGLGDAFHMGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPE 180

QY 170 PVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVD 229
DB 181 PVTVSNNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVD 240

QY 230 KVKPKSCDKHTCTCPCP----- 247
DB 241 KVKPKSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE 300
QY 248 ----- 247
DB 301 VKFNWTVYDGVVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPI 360

QY 248 -----GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNYK 299
DB 361 EKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNYK 420

QY 300 TTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHHTQKSLSLSPGK 354

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Db 421 TTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHHTQKSLSLSPGK 475

RESULT 6
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobott G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.8%; Score 1440; DB 2; Length 472;
Best Local Similarity 59.3%; Pred. No. 2.2e-95;
Matches 280; Conservative 33; Mismatches 41; Indels 118; Gaps 2;

QY 1 MGSLLILLFLVAVATVLSQVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
DB 1 MELGLTWFLAILKGVQCVQLVESGGGLVQPGSRSLRSTASGTFDIDYAMHWVRQAP 60

QY 61 GORLEWIGYFSPGNDPFKYNRFKGNATLTADTSASTAYVELSLRSEDVAVYFCTRSL- 119
DB 61 GKGLEWVSGISWNISGSIAYADSVKGRFTISRDNKNSLYLQNSLRAEDTALYYCAKEIG 120

QY 120 -----NNAYWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEVPT 172
DB 121 AHNFYVYGVDMVQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEVPT 180

QY 173 VSNWSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVV 232
DB 181 VSNWSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVV 240

QY 233 EPKSCDKHTCTCPCP----- 247
DB 241 EPKSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 300
QY 248 ----- 247
DB 301 NWVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 360

QY 248 -----GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNYK 302
DB 361 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNYK 420

QY 303 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHHTQKSLSLSPGK 354

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QY 248 ----- 247
Db 301 VKFNWYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360
QY 248 -----GOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 299
Db 361 EXTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420
QY 300 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 354
Db 421 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 475

RESULT 9
Q6PJ95 HUMAN
ID Q6PJ95 HUMAN PRELIMINARY; PRT; 544 AA.
AC Q6PJ95
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -, mRNA.
DR HSSP; P01861; 1A0Q.
DR SWR; Q6PJ95; 20-473.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2237C668 CRC64;

Query Match 76.1%; Score 1427.5; DB 2; Length 544;
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Best Local Similarity 59.6%; Pred. No. 2.1e-94;
Matches 282; Conservative 28; Mismatches 42; Indels 121; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVOSGAEVVKPGASVKISKASGYTTDTHAIHWKQP 60
Db 1 MFGSLSVFLVALLRGVQCAQLVSGGVVQVPGSSLRSLSCAASGFRFSNYGMHWVQAP 60
QY 61 GQRLIEWGFSPGNDDFKYNRPFKCATLTADTSATAYVELSSLRSSEDTAVYFCTRS-- 118
Db 61 KGLEWAVAFVSDESKYAAASVKGRFTISRNSKNLTSLQNSLRVEDTAVYICAKOOK 120
QY 119 -----LNMYMGQGLTVTVSSASTKGPSVFFPLAPSSKTSSTGTAALGCLVKDYFPE 169
Db 121 PMSNSWFLTFNDSWGRGLTVTVSSASTKGPSVFFPLAPSSKTSSTGTAALGCLVKDYFPE 180
QY 170 PVTSMNSGALTSGVHTTFAVLQSSGLYSLSVTVTPSSSLGTQYIYCNVNHKPSNTKVD 229
Db 181 PVTSMNSGALTSGVHTTFAVLQSSGLYSLSVTVTPSSSLGTQYIYCNVNHKPSNTKVD 240
QY 230 KKVEPKSCDKTHTCPCP----- 247
Db 241 KKVEPKSCDKTHTCPCPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300
QY 248 ----- 247
Db 301 VKFNWYVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360
QY 248 -----GOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 299
Db 361 EXTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYK 420
QY 300 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSP 352
Db 421 TTPPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSP 473

RESULT 10
Q6IN78 HUMAN
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -, mRNA.
DR HSSP; P01861; 1A0Q.
DR SWR; Q6PJ95; 20-473.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2237C668 CRC64;

"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RG TISSUE=Peripheral Nervous System;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCEDE81076E CRC64;

Query Match 76.0%; Score 1426; DB 2; Length 466;
Best Local Similarity 60.4%; Pred. No. 2.2e-94;
Matches 282; Conservative 30; Mismatches 41; Indels 114; Gaps 3;

QY 1 MGWSLLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHVKWQNP 60
Db 1 MEFWLSWVFLVAILKGVOCEVLVESGGGLIQPGLSLTLSCAASGLTVSSNVMHWVRQAP 60
QY 61 GQRLWIGVYFSGNDDFKYNERRFKGKATLTADTSASTAYVELSLRSSEDTAVYFCTRS-- 118
Db 61 GKGLWVSVLYIGGARY-YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYICARGNY 119
QY 119 -LNMAVWGQTLTVTSASSTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNS 177
Db 120 VVPAAPWGQTLTVTSASSTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNS 179
QY 178 GALTSGVHTFPFPAVLQSSGLYSLSVSVTVFSSSLGTQTYICNVNHPKSNKTKVDKVPKSC 237
Db 180 GALTSGVHTFPFPAVLQSSGLYSLSVSVTVFSSSLGTQTYICNVNHPKSNKTKVDKVPKSC 239
QY 238 DKTHCTCPPCP----- 247
Db 240 DKTHCTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVVDVSHEDPEVKFNMYD 299
QY 248 ----- 247
Db 300 GVEVHNATKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 359
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLD 307
Db 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLD 419
QY 308 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALNHYTQKSLSPGK 354
Db 420 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALNHYTQKSLSPGK 466

RESULT 11
Q6PUJ4 HUMAN
ID Q6PUJ4 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PUJ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
QY 305 LPSDSGFFLYSKLTVDKSRWQQGNVSCSVMHEALNHHYTKQSLSLSPGK 354
Db 421 LPSDSGFFLYSKLTVDKSRWQQGNVSCSVMHEALNHHYTKQSLSLSPGK 470

RESULT 12
Q6GMW7 HUMAN
ID Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 75.8%; Score 1422.5; DB 2; Length 475;
Best Local Similarity 59.6%; Pred. No. 4e-94;
Matches 283; Conservative 28; Mismatches 43; Indels 121; Gaps 3;

QY 1 MGMSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHHWKQNP 60
Db 1 MEFGLSCVFLVAIFKGVHCEVQLVESGGGLVQPGSLRLSCVASFITLSRHAHWVRQAP 60
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QY 61 GORLEWIGVSPGNDDFKYNRFK GKATLTADTSASTAYVELSSLRSSEDTAVYFCTRS-- 118
Db 61 KGLEYVSGISNSENSTYIADSVKGRFTISRDNYKNTLYLQLGSURAEKAVYYCARARC 120
QY 119 -----LNMA-----WGQGTTLVTVSSASTKGPSVFPLPAPSSKTSKSTGTAALGCLVKDYFPE 169
Db 121 RGDTCCLNFYGLDVMVGQGTIVVSSASTKGPSVFPLPAPSSKTSKSTGTAALGCLVKDYFPE 180
QY 170 PVTVSNWNGALTSVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHHKPSNTKYD 229
Db 181 PVTVSNWNGALTSVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHHKPSNTKYD 240
QY 230 KKVEPKSCDKTHHTCPPCP----- 247
Db 241 KKVEPKSCDKTHHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPE 300
QY 248 ----- 247
Db 301 VKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 299
Db 361 EXTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 420
QY 300 TTPPVLDSDGSFPLYSKLTVDKSRWQQGNVSCSVMHEALNHHYTKQSLSLSPGK 354
Db 421 TTPPVLDSDGSFPLYSKLTVDKSRWQQGNVSCSVMHEALNHHYTKQSLSLSPGK 475

RESULT 13
Q6N096 HUMAN
ID Q6N096 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15196.
GN Names=DKFZp686I15196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RA The German CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAE45774.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6N096; 20-466.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D57C4 CRC64;

Query Match 75.5%; Score 1417; DB 2; Length 466;
Best Local Similarity 60.3%; Pred. No. 9.8e-94;
Matches 281; Conservative 28; Mismatches 45; Indels 112; Gaps 2;

QY 1 MGMSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHHWKQNP 60
```



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Db 1 MERGLSVFLVAILKGVQCQVQLVQSGAEVVKPGASVKISCKASGVTFTDHAHWKQNP 60
QY 61 GORLEWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSRSEDVAVYFCTRS 118
Db 61 GKGVLVWSLNRDASSETAYAEFVQGRFTISRDNKNTLFLQLSLRAEDVAVYCARGF 120
QY 119 LNMYAGQGGLTVTVSSASTKGPSVFPPLAPSKTSKSGTAAALGCLVKDYFPEPVTVMNSG 178
Db 121 GNFDWQGGTLVTVSSASTKGPSVFPPLAPSKTSKSGTAAALGCLVKDYFPEPVTVMNSG 180
QY 179 ALTSVGHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKEPKSCD 238
Db 181 ALTSVGHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKKEPKSCD 240
QY 239 KHTHCPDPCP----- 247
Db 241 KHTHCPDPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 300
QY 248 -----G 248
Db 301 VEHNNAKTPREBQYNSTYRVWSVLTVLHODWLNGKEYKCRVSNKALPAPIEKTISKAKG 360
QY 249 QPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSD 308
Db 361 QPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSD 420
QY 309 GSFFLYSKLTVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db 421 GSFFLYSKLTVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 466
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## RESULT 14

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Q5RE17_PONPY
ID Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKF2p469C2335.
GN Name=DKF2p469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Kidney;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CB857722; CAH8990.1; -; mRNA.
DR SRR; Q5RE17; 21-475.
DR GO; GO:0030106; F.MHC class I receptor activity; IEA.
DR GO; GO:0019883; P-antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P-antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51898 MW; 04BDBE096A2CD529 CRC64;
```

Query Match

75.2%; Score 1411.5; DB 2; Length 475;

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Best Local Similarity 58.6%; Pred. No. 2.5e-93;
Matches 279; Conservative 32; Mismatches 42; Indels 123; Gaps 3;
QY 1 MGWSLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGVTFTDHAHWKQNP 60
Db 1 MGFVSLALLAVLQACADIQLVQSGAEVVKRFGESLRISCKSGVTFTDHWLWGRQMP 60
QY 61 GORLEWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSRSEDVAVYFCTRS 120
Db 61 GKGLELMGMIDPSNSGTYKYNRSPEGHITTSADMSISTAYLQMTSLKASDAIYCAR-LR 119
QY 121 MA-----YNGQGLTVTVSSASTKGPSVFPPLAPSKTSKSGTAAALGCLVKDYF 168
Db 120 LSGTNSYHKRSYFQFVGQGLTVLVSASTKGPSVFPPLAPSSRSTSGTAAALGCLVKDYF 179
QY 169 EPTVSWNSGALTSVGHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 228
Db 180 EPTVSWNSGALTSVGHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 239
QY 229 DKKVEPKSCDKHTHCPDPC----- 247
Db 240 DKKVEPKSCDTPRCPDPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDP 299
QY 248 ----- 247
Db 300 EVKFNWYVDGEVHNNAKTPREBQYNSTYRVWSVLAVHODWLNGKEYKCRVSNKALPAP 359
QY 248 -----GPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNY 298
Db 360 IEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESGQPENNY 419
QY 299 KTTTPVLDSDGSGFFLYSKLTVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db 420 KTTTPVLDSDGTFPFLYSKLTVDSKRWQGNIFSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 15
Q6PI81_HUMAN
ID Q6PI81_HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McQuellano J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
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Search completed: February 16, 2006, 10:22:53  
Job time : 186.96 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1127.5	60.1	469	2	S37483	Ig gamma-2a chain C
2	1116	59.5	330	1	GHHU	Ig gamma-1 chain C
3	1094	58.3	446	2	S40295	Ig gamma-2a chain
4	1066	56.8	474	1	G2NS11	Ig gamma-2b chain
5	1030.5	54.9	326	2	S01321	Ig gamma-2b chain
6	1006	53.6	326	1	G2HU	Ig gamma-2 chain C
7	997.5	53.2	377	2	A23511	Ig gamma-3 chain C
8	995.5	53.1	377	2	A60764	Ig gamma-3 chain C
9	981.5	52.3	444	2	PC4436	monoclonal antibody
10	974.5	51.9	327	1	G4HU	Ig gamma-4 chain C
11	946	50.4	470	2	S22080	Ig heavy chain pre
12	940	50.1	472	2	S31459	Ig gamma-1 chain -
13	852	45.4	374	2	S69339	Ig heavy chain V r
14	814.5	43.4	241	2	S68131	Ig heavy chain (DO
15	809	43.1	246	2	S38950	Ig gamma chain - m
16	803.5	42.8	249	2	S69340	Ig heavy chain VHR
17	777	41.4	220	2	A49444	Ig gamma-1 heavy c
18	769	41.0	548	2	S38864	Ig epsilon chain C
19	748	39.9	218	2	A36040	Ig heavy chain V-I
20	737	39.3	328	2	I47159	Ig gamma-2a chain
21	733	39.1	328	2	I47158	Ig gamma-1 chain c
22	732	39.0	328	2	I47161	Ig gamma-3 chain c
23	731	39.0	328	2	I47160	Ig gamma-2b chain
24	726	38.7	214	2	PC4202	monoclonal antibody
25	722.5	38.5	323	1	GHRB	Ig gamma chain C r
26	722	38.5	322	2	PS0019	Ig gamma-2a chain
27	720	38.4	326	2	PS0017	Ig gamma-1 chain C
28	715.5	38.1	221	2	S49220	Ig gamma-1 chain -
29	707	37.7	549	2	S04845	Ig heavy chain pre

Db 419 VLDSGYSFYMSKLRVEKQWVNRNSYSCSVVHEGLNHHHTTKSFSPGK 469

RESULT 2

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A>Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAP>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-1137235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', '98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A>Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,

A:Cross-references: UNIPARC:UPI000017378E

A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27

A:Cross-references: UNIPARC:UPI000017378F

A>Note: this sequence has the G1m(17) and G1m(1) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983

A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI

A:Reference number: A91723; MUID:83289131; PMID:6884994

A:Contents: myeloma protein KOI; disulfide bonds

A:Accession: A91723

A:Molecule type: protein

A:Residues: 1-96, 'R', '98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH

A:Cross-references: UNIPARC:UPI0000173790

A>Note: this sequence has the G1m(3) and G1m(non-1) markers

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfu

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; disulfide bonds

R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

enonide cleavage products, and the disulfide bridges.

A:Reference number: A91667; MUID:77070267; PMID:1002129

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 9/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:137-206/Domain: immunoglobulin homology <IM2>

F:243-310/Domain: immunoglobulin homology <IM3>

F:27-83,144-204,250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental

F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 59.5%; Score 1116; DB 1; Length 330;

Best Local Similarity 66.7%; Pred No. 1.4e-60;

Matches 220; Conservative 0; Mismatches 0; Indels 110; Gaps 1;

QY 135 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 194

|||||

Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSS 60

|||||

QY 195 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHHTCPPCP----- 247

|||||

Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHHTCPPCPAPPELLGG 120

|||||

QY 248 ----- 247

Db 121 PSVFLFPKPDKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

QY 248 -----GQPREPQVYTLPPSRDE 264

Db 181 STYRVSVLTVLHQDLNGLKEYCKVKNKALPAPIEKTISKAKGQPREPVYTLPPSRDE 240

QY 265 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 324

|||||

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

QY 325 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 354

Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 3

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text\_change 09-Jul-2004

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B

C:Accession: S40295

submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

A:Cross-references: UNIPROT:Q99L25; UNIPARC:UPI0000176F38

A:Reference number: A02157; MUID:80120716; PMID:6766534  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161,'L','163-189','FP','193-474 <YAM>  
A:CROSS-references: UNIPARC:UPI00000272D2; GB:J00461  
A>Note: The sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he-  
A:Reference number: A26235; MUID:80081501; PMID:117548  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172,'P','174-189','FP','193-376','T','378-474 <TU1>  
A:CROSS-references: UNIPARC:UPI00001737AF  
A>Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain  
A:Reference number: A26232; MUID:80081502; PMID:117549  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172,'P','174-189','FP','193-376','T','378-474 <TU2>  
A:CROSS-references: UNIPARC:UPI00001737AF  
R:Oillo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chains  
A:Reference number: A26233; MUID:82173203; PMID:6803173  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161,'L','163-189','FP','193-300','R','302-331','A','333-437','DI','440-474 <OLL>  
A:CROSS-references: UNIPARC:UPI00001737B0; GB:J00461  
R:Kim, H.; Yanaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, T.  
J. Biol. Chem. 269, 12345-12350, 1994  
A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359; PMID:7512967  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KM>  
A:CROSS-references: UNIPARC:UPI00001737B1  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:1 ratio.  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.8%; Score 1066; DB 1; Length 474;  
Best Local Similarity 45.6%; Pred. No. 2.1e-57;  
Matches 216; Conservative 49; Mismatches 89; Indels 120; Gaps 4;

Qy 1 MGHSLLLEFLVAVATRVLSQVLVSQGAEEVKISCKASGYTFDTDAIHWWKQP 60  
Db 1 MEWSWIFLFLLSGTAGHSEVQLQQSGPELVNPGSVKMSCKASGYTFITYNVHWYKQP 60  
Qy 61 GQRLEWIGYSPGNDDFPKYNREFKGKATLTADTSAGTAYVELSSLRSSEDTAVVFCTRLN 120  
Db 61 GGGLIEWIGYNPNKDGTGFNEKEFGKATLT3DKSSNTAYVELSSLTSSEDSANYYCARDYD 120  
Qy 121 ---MAYWGQGLTVTVSSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYFPPETVSWNS 177



hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:133-202/Domain: immunoglobulin homology <IM2>  
 F:239-306/Domain: immunoglobulin homology <IM3>  
 F:14/bisulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,140-200,246-304/bisulfide bonds: #status experimental  
 F:102,103,106,109/bisulfide bonds: interchain (to heavy chain) #status experimental  
 F:176/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 53.6%; Score 1006; DB 1; Length 326;  
 Best Local Similarity 61.1%; Pred. No. 6e-54; Indels 112; Gaps 2;  
 Matches 201; Conservative 7; Mismatches 9;

QY 135 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 194  
 DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKVPKSCDKTHTCPPCP----- 247  
 DB 61 GLYSLSVVTVPSNFGTTQYICNVDHKPSNTKVDKTKVERKCCVE---CPPCPAPPVAGP 117

QY 248 ----- 247

DB 118 SVFLFPKPDTLMISRTPEVTCVVVDVSHEDPEVFQWYVDGVEVHNNAKTKPREBQFNS 177

QY 248 -----GQPREPOVYTLPPSRDEL 265

DB 178 TRVVSVLTVMHQDLNGKEYCKVSKNKGKLPAPIEKTIISKTKGQPREPOVYTLPPSRDEM 237

QY 266 TKNQVSLTCLVGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDSGFFLYSKLTVDKSRWQ 325  
 DB 238 TKNQVSLTCLVGFYPSDIAVEWESNGQPENNYKTTTPPMLDSGDSGFFLYSKLTVDKSRWQ 297

QY 326 QGVFSCSVMEALHNHYTQKSLSLSPGK 354  
 DB 298 QGVFSCSVMEALHNHYTQKSLSLSPGK 326

RESULT 7

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
 C:Accession: A23511  
 R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
 Nucleic Acids Res. 14, 1779-1789, 1986  
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c  
 A:Reference number: A23511; MUID:86148507; PMID:3081877  
 A:Accession: A23511  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272  
 C:Genetics:  
 A:Gene: GDB:IGHG3  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM>

Query Match 53.2%; Score 997.5; DB 2; Length 377;  
 Best Local Similarity 53.8%; Pred. No. 2.3e-53; Indels 157; Gaps 2;  
 Matches 203; Conservative 8; Mismatches 9;

QY 135 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 194  
 DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKKV----- 232

DB 61 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKVELKTPGLDTHTCRCRCPKSC 120

QY 233 -----EPKSCDKTHTCPPCP----- 247

DB 121 DTTPPCRCRCPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGGPSVFLFPPPKDPT 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQWYVDGVEVHNNAKTKPREEQYNSTFRVVSULTVLH 240

QY 248 -----GQPREPOVYTLPPSRDELTKNOVSLTCLVK 277

DB 241 QDLNGKEYCKVSKNKAAPAPIEKTIISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 337

DB 301 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354  
 DB 361 ALHNRTQKSLSLSPGK 377

DB 61 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKVELKTPGLDTHTCRCRCPKSC 120

QY 233 -----EPKSCDKTHTCPPCP----- 247

DB 121 DTTPPCRCRCPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGGPSVFLFPPPKDPT 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQWYVDGVEVHNNAKTKPREEQYNSTFRVVSULTVLH 240

QY 248 -----GQPREPOVYTLPPSRDELTKNOVSLTCLVK 277

DB 241 QDLNGKEYCKVSKNKAAPAPIEKTIISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 337

DB 301 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354  
 DB 361 ALHNRTQKSLSLSPGK 377

RESULT 8

A60764

Ig gamma-3 chain C region, form LAT - human  
 C:Species: Homo sapiens (man)  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
 C:Accession: A60764  
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conver  
 A:Reference number: A60764; MUID:90007613; PMID:2571587  
 A:Accession: A60764  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B  
 C:Superfamily: immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM>

Query Match 53.1%; Score 995.5; DB 2; Length 377;  
 Best Local Similarity 53.8%; Pred. No. 3e-53; Indels 157; Gaps 2;  
 Matches 203; Conservative 8; Mismatches 9;

QY 135 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 194  
 DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKKV----- 232

DB 61 GLYSLSVVTVPSSSLGTTQYICNVNHKPSNTKVDKVELKTPGLDTHTCRCRCPKSC 120

QY 233 -----EPKSCDKTHTCPPCP----- 247

DB 121 DTTPPCRCRCPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGGPSVFLFPPPKDPT 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQWYVDGVEVHNNAKTKPREEQYNSTFRVVSULTVLH 240

QY 248 -----GQPREPOVYTLPPSRDELTKNOVSLTCLVK 277

DB 241 QDLNGKEYCKVSKNKAAPAPIEKTIISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVK 300

QY 278 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 337

DB 301 GYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQGNVFSVCSVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354  
 DB 361 ALHNRTQKSLSLSPGK 377

RESULT 9  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
A:Accession: PC4436  
R:Kashii, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JCS810; MUID:98063277; PMID:9398605  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
A:CROSS-references: UNIPARC:UPI0000176F41  
C:Comment: This catalytic antibody has peroxidase activity. It is directed against  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 52.3%; Score 981.5; DB 2; Length 444;  
Best Local Similarity 41.9%; Pred. No. 2.5e-52;  
Matches 188; Conservative 66; Mismatches 76; Indels 119; Gaps 5;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQRLEWIGYFSPGNDPF-- 77  
DB 1 EVQVETGGGLVRPGNSLKSLCSTGFTFSNYRMHWLRQPPGKRLIEWIAIVTKSDNYGA 60

QY 78 KNERPKGKATLTADTSASTAVEVLSLSRSDTAVYFCFTR---LNMYWGQGLTVVSS 134  
DB 61 KYAESVRGRTISRDDSKSVYLQNNRLREEDTATYICCTTPWVAMDCMGQGSTIVSS 120

QY 135 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSMNSGALTSGVHTFPVQLQS 194  
DB 121 AKTTPSVVPLAPGSAQNSWVTLGCLVKGFPEPTVSMNSGSLSSGVHTFPVQLQSD 180

QY 195 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 246  
DB 181 -LYTLSSVTVSPSTWPSSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEVS 235

QY 247 ----- 246

DB 236 SVFIFFPKPDVLTITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREBQFNS 295

QY 247 -----PQPREQVTVTLPPSRDEL 265  
DB 296 TFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEKTIKTKGRPKAPQVYTIIPPKQEM 355

QY 266 TRNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQ 325  
DB 356 AKDKVSLTCWITDFPEDITVEWQNGQPAENYKNTQPTMDTDSGYFYVTKLVNQKSNWE 415

QY 326 QGNVFCSCVMHEALHNHYTKSLSPGK 354  
DB 416 AGNTFTCSVLHLEGLHNHHTKSLSHSPGK 444

RESULT 10  
GHU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
A:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:CROSS-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A>Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
A:CROSS-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:CROSS-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 9/1; 11/1; 22/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 974.5; DB 1; Length 327;  
Best Local Similarity 59.7%; Pred. No. 4.8e-52;  
Matches 197; Conservative 9; Mismatches 11; Indels 113; Gaps 2;

QY 135 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSMNSGALTSGVHTFPVQLQS 194  
DB 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVSMNSGALTSGVHTFPVQLQS 60

QY 195 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 247  
DB 61 GLYSLSSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKVPKSCDKTHTCPPC----- 117

QY 248 ----- 247

DB 118 PSVFLPPPKDPTLMISRTPEVTCTVVDVDSQBDPEVQFNWYVDGVEVHNKTKPREEQFN 177

QY 248 -----GOPREQVTVTLPPSRDE 264  
DB 178 STYRVSVLTUHQDWLNGKEYKCVSKNGLPSSEKTKSKAGQPREQVTVTLPPSQEE 237

QY 265 LTKNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 324  
DB 238 MTKNQVSLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSPFLYSRLTVDKSRW 297

QY 325 QGNVFCSCVMHEALHNHYTKSLSPGK 354  
DB 298 QEGNVFCSCVMHEALHNHYTKSLSLGK 327

RESULT 11  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:CROSS-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989





Db 127 YRPSHWGQGLTVVTSSEPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDGLMIKRTPEV 186

QY 160 GCLVKDYFPEPVTVSWN---SGALTSGVHFTFAVLQSSGLYSLSSVTVTPSSS-LGTQTY 215

Db 187 TCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEY 246

QY 216 ICNVNHHKPSNTKVDKKVPEKSCDKTHTCPCPGQPREPOVYTLPPSRDELTKNOVSLTCL 275

Db 247 KCKVSNKALPAPIEK-----TISKAGQPREPOVYTLPPSREEMTKNQVSLTCL 295

QY 276 VKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVM 335

Db 296 VKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRWQQGNVFCSSVM 355

QY 336 HEALHNHYTQKSLSLSPGK 354

Db 356 HEALHNHYTQKSLSLSPGK 374

RESULT 14

S69131

Ig heavy chain (DOT) - human (fragment)

N:Alternate names: anti-riboflavin IgG Fd fragment

C:Species: Homo sapiens (man)

C>Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000

C:Accession: S69131

R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.

Eur. J. Biochem. 228, 886-893, 1995

A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins

F:140-205/Domain: immunoglobulin homology <IMM>

A:Reference number: S69130; MUID:95255298; PMID:7737190

A:Accession: S69131

A:Molecule type: protein

A:Residues: 1-241 <STO>

A:Cross-references: UNIPARC:UPI0000176F40

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid

F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>

F:140-205/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 43.4%; Score 814.5; DB 2; Length 241;

Best Local Similarity 66.8%; Pred. No. 1.6e-42;

Matches 163; Conservative 23; Mismatches 47; Indels 11; Gaps 4;

QY 20 QVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 79

Db 1 QVLVQSGVERKVPAGASVRIKSKASGYAFENYIHWVQAPGLGLEWMGIFNPVAGAVS- 59

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTR-----SLNMAWVGQGLTVTVS 133

Db 60 SEKFRDLVNSDTSANTVSMQLNRKSDDTGRYFCARVSYDFSQYGMVWGQGLTVTVS 119

QY 134 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 193

Db 120 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 179

QY 194 SGLYSLSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPGQ 252

Db 180 SGLYSLSVTVTPSSNFGITQTYICNVDHKPSNTKVDKVERKCCVE---CPPCPAPPVAG 236

QY 253 PQVY 256

Db 237 PSVF 240

RESULT 15

S38950

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi

Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IGG2a antibody mAb735 against alpha

A:Reference number: S38950; MUID:94128242; PMID:8297501

A:Accession: S38950

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLS>

A:Cross-references: UNIPARC:UPI0000176F3B

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 809; DB 2; Length 246;

Best Local Similarity 64.4%; Pred. No. 3.6e-42;

Matches 159; Conservative 28; Mismatches 52; Indels 8; Gaps 4;

QY 20 QVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 79

Db 1 QILOQSGPELVKPGASVKISKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 60

QY 80 NERFKGKATLTADTSASTAYVELSLRSEDATVYFCTR--SLNMAWVGQGLTVTVSSAST 137

Db 61 NEKFKGKATLTVDTSSTAYMQLSLTSDSAVFCARGGKFAMDYWGQGLTVTVSSAKT 120

QY 138 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSSGLY 197

Db 121 TAPSVYPLAPVCGDTTGGSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD-LY 179

QY 198 SLSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPC----PGQPREP 253

Db 180 TLSSSVTVTSTWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPPCKCPAPNLLGGP 238

QY 254 QVYTLPP 260

Db 239 SVFIPPP 245

Search completed: February 16, 2006, 10:23:48

Job time : 31.798 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:12:02 ; Search time 194.879 Seconds  
(without alignments)  
798.138 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSILFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876	100.0	354	5	Aae27926 Human CH2
2	1876	100.0	354	6	Abb82835 Antibody
3	1770	94.3	347	9	Adw77045 Heavy cha
4	1763.5	94.0	360	9	Adw77049 Heavy cha
5	1762.5	93.9	362	9	Adw77050 Heavy cha
6	1762.5	93.9	603	9	Adw44587 Antibody
7	1762.5	93.9	621	9	Adw44588 Antibody
8	1755.5	93.6	362	9	Adw77053 Heavy cha
9	1683	89.7	360	5	Aae27924 Human CH2
10	1683	89.7	360	6	Abb82833 Antibody
11	1614	86.0	470	5	Aae27923 Human C2B
12	1614	86.0	470	6	Abb82832 Antibody
13	1613.5	86.0	731	4	Aam52156 Humanised
14	1613.5	86.0	741	4	Aam52159 Humanised
15	1613	86.0	470	3	Aab08026 A dimeric
16	1608.5	85.7	729	4	Aam52158 Humanised
17	1608.5	85.7	739	4	Aam52161 Humanised
18	1608	85.7	462	9	Aeb080800 Anti-NOGO
19	1604	85.5	464	8	Adu68011 Mouse ant
20	1603	85.4	470	3	Aaw83036 Anti-Fas
21	1603	85.4	470	2	Aab14776 Humanised
22	1603	85.4	470	3	Aaw90926 Humanised
23	1603	85.4	470	3	Abb74941 Humanised
24	1603	85.4	470	5	Abb74895 Humanised

RESULT 1

AAE27926	AAE27926 standard; protein; 354 AA.
XX	AAE27926;
AC	AAE27926;
XX	
DT	27-DEC-2002 (first entry)
XX	
DE	Human CH2 domain deleted CC49 antibody heavy chain protein.
XX	
KW	Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW	neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW	non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX	
OS	Homo sapiens.
XX	
PN	WO200260955-A2.
XX	
PD	
XX	08-AUG-2002.
XX	
PF	29-JAN-2002; 2002WO-US002373.
XX	
PR	29-JAN-2001; 2001US-0264318P.
PR	16-NOV-2001; 2001US-0331481P.
PA	(IDEC-) IDEC PHARM CORP.
PI	Braclawsky GR, Hanna N, Chinn P;
DR	WPI; 2002-698547/75.
XX	N-PSDB; AAD45755.
XX	
PT	Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT	-72, or C2B8 antibody reactive with CD20, useful for treating
PT	myelosuppressed patient suffering from a neoplastic disorder.
PS	Example 2; Fig 4A; 74pp; English.
CC	The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC	Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC	deleted sequence in which CH2 domain has been deleted and are reactive
CC	with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC	with CD20 and comprise a heavy chain having a sequence of a derived
CC	domain deleted C2B8 construct where the CH2 domain has been deleted.
CC	Sequences of the invention are useful for imaging a neoplasm. They are
CC	also useful for treating myelosuppressed patients suffering from
CC	neoplastic disorder such as haematologic neoplasm, preferably non-

CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
CC useful for reducing tumour size, inhibiting tumour growth and/or  
CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CH2 domain deleted CC49 antibody  
CC heavy chain protein. This sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 354 AA;  
Query Match 100.0%; Score 1876; DB 5; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.2e-114; Indels 0; Gaps 0;  
Matches 354; Conservative 0; Mismatches 0;  
QY 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
DB 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
QY 61 GORLEWIGYFSPGNDPFKNRPFKATLTADTSASTAYVELSLRSEDYVYFCTRSIN 120  
DB 61 GORLEWIGYFSPGNDPFKNRPFKATLTADTSASTAYVELSLRSEDYVYFCTRSIN 120  
QY 121 MAYWQGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180  
DB 121 MAYWQGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180  
QY 181 TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKT 240  
DB 181 TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKT 240  
QY 241 HTCPPCPGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
DB 241 HTCPPCPGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
QY 301 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
RESULT 2  
ID ABB82835  
XX ABB82835 standard; protein; 354 AA.  
AC ABB82835;  
XX  
XX 31-MAR-2003 (first entry)  
XX  
DE Antibody huCC49 CH2 domain deleted heavy chain.  
XX  
XX CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX WO200296948-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002374.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
PR 21-DEC-2001; 2001US-0341858P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;  
PI WPI; 2003-140446/13.  
XX  
DR N-PSDB; AB224019.  
DR

XX  
PT Novel dimeric antibody useful for treating immune disorder and neoplastic  
PT disorder, has several non-covalently associated monomeric subunits.  
XX  
XX Example 1; Fig 4A; 78pp; English.  
XX  
XX The invention relates to a dimeric antibody (I) comprising several  
CC monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (iPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
CC represents the antibody huCC49 CH2 domain deleted heavy chain  
XX  
SQ Sequence 354 AA;  
Query Match 100.0%; Score 1876; DB 6; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.2e-114; Indels 0; Gaps 0;  
Matches 354; Conservative 0; Mismatches 0;  
QY 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
DB 1 MGWSLILLFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQP 60  
QY 61 GORLEWIGYFSPGNDPFKNRPFKATLTADTSASTAYVELSLRSEDYVYFCTRSIN 120  
DB 61 GORLEWIGYFSPGNDPFKNRPFKATLTADTSASTAYVELSLRSEDYVYFCTRSIN 120  
QY 121 MAYWQGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180  
DB 121 MAYWQGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGAL 180  
QY 181 TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKT 240  
DB 181 TSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKT 240  
QY 241 HTCPPCPGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
DB 241 HTCPPCPGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300  
QY 301 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 TTPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
RESULT 3  
ADW77045  
ID ADW77045 standard; protein; 347 AA.  
XX  
XX ADW77045;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Heavy chain CH2 domain-deleted huCC49 polypeptide #1.  
XX  
XX Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;  
KW antiinflammatory; antiulcer; gastrointestinal-gen.; neoplasm;



CC polypeptide chain, a host cell comprising the nucleic acid molecule, a  
CC connecting peptide, a domain deleted antibody molecule, an antibody  
CC molecule, a method of separating a first properly folded antibody  
CC molecule from a second improperly folded antibody molecule, where each of  
CC the first and second antibody molecules comprises four polypeptide  
CC chains, where at least two of the chains comprise at least one heavy  
CC chain portion, and at least two of the chains comprise at least one light  
CC chain portion, a method of increasing the amount of a first polypeptide  
CC dimer relative to the amount of a second polypeptide dimer produced by a  
CC cell, a composition comprising a first polypeptide dimer, a polypeptide  
CC comprising a synthetic connecting peptide, where the polypeptide is not a  
CC naturally occurring IgG3 molecule, and a method of increasing the amount  
CC of dimers comprising polypeptide chains linked via at least one disulfide  
CC linkage in a population of IgG4 molecules produced by a cell. The  
CC composition is useful for treating a subject that would benefit from  
CC treatment with a binding molecule, where the subject is suffering from  
CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory  
CC disease or disorder. The autoimmune diseases include Crohns disease,  
CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative  
CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,  
CC Hashimotos disease, pemphigus vulgaris, myasthenia gravis, scleroderma,  
CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.  
CC This sequence represents a heavy chain CH2 domain-deleted huCC49  
CC polypeptide, used in the scope of the invention.

XX Sequence 360 AA;

Query Match 94.0%; Score 1763.5; DB 9; Length 360;  
Best Local Similarity 93.1%; Pred. No. 2.8e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 25; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPQORLEWIGYFSGNDDPKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPQORLEWIGYFSGNDDPKY 60  
QY 80 NERFVGKATLTADTASTAYVELSLRSBDAVYFCTSLNWAYWGQGLTVTVSSASTKG 139  
DB 61 NERFVGKATLTADTASTAYVELSLRSBDAVYFCTSLNWAYWGQGLTVTVSSASTKG 120  
QY 140 PSVFPLAPSSKSTSGTGAALGLVVDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPLAPSSKSTSGTGAALGLVVDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 180  
QY 200 SSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPCP----- 247  
DB 181 SSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTCPCP----- 240  
QY 248 -----GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 RCPGGSGSGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300  
QY 295 ENNYKTTTPVLDSGDFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSGDFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 5  
ADW77050  
ID ADW77050 standard; protein; 362 AA.

XX ADW77050;

XX 24-MAR-2005 (first entry)

XX Heavy chain CH2 domain-deleted huCC49 polypeptide #3.

DE Protein production; protein purification; cancer; lymphoma;  
DE autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimotos disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;

KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;  
KW antiinflammatory; antidiabetic; gastrointestinal-gen.; neoplasm;  
KW immune disorder; huCC49; heavy chain; antibody.

XX Homo sapiens.  
OS Synthetic.

XX WO2005000898-A2.

XX 06-JAN-2005.

XX 28-JUN-2004; 2004WO-US020944.

XX 27-JUN-2003; 2003US-0483877P.

XX 03-OCT-2003; 2003US-0508810P.

XX 28-OCT-2003; 2003US-0515351P.

XX 30-OCT-2003; 2003US-0516030P.

XX (BT0G-) BIOGEN IDEC MA INC.

XX Braslawsky GR, Glaser S, Yang T, Hopp J, Chinn P;

XX WPI; 2005-058132/06.

XX N-PSDB; ADW77048.

XX Claim 30; SEQ ID NO 23; 152pp; English.

CC The invention relates to a composition comprising polypeptide dimers  
CC having at least two binding sites and at least two polypeptide chains,  
CC where the polypeptide chains comprise at least one heavy chain portion  
CC and a synthetic connecting peptide. The invention also relates to a  
CC nucleic acid molecule comprising a nucleotide sequence encoding a  
CC polypeptide chain, a host cell comprising the nucleic acid molecule, a  
CC connecting peptide, a domain deleted antibody molecule, an antibody  
CC molecule, a method of separating a first properly folded antibody  
CC molecule from a second improperly folded antibody molecule, where each of  
CC the first and second antibody molecules comprises four polypeptide  
CC chains, where at least two of the chains comprise at least one heavy  
CC chain portion, and at least two of the chains comprise at least one light  
CC chain portion, a method of increasing the amount of a first polypeptide  
CC dimer relative to the amount of a second polypeptide dimer produced by a  
CC cell, a composition comprising a first polypeptide dimer, a polypeptide  
CC comprising a synthetic connecting peptide, where the polypeptide is not a  
CC naturally occurring IgG3 molecule, and a method of increasing the amount  
CC of dimers comprising polypeptide chains linked via at least one disulfide  
CC linkage in a population of IgG4 molecules produced by a cell. The  
CC composition is useful for treating a subject that would benefit from  
CC treatment with a binding molecule, where the subject is suffering from  
CC cancer, lymphoma, an autoimmune disease or disorder or an inflammatory  
CC disease or disorder. The autoimmune diseases include Crohns disease,  
CC inflammatory bowel disease, systemic lupus erythematosus, ulcerative  
CC colitis, rheumatoid arthritis, Goodpasture's syndrome, Grave's disease,  
CC Hashimotos disease, pemphigus vulgaris, myasthenia gravis, scleroderma,  
CC autoimmune hemolytic anemia, pernicious anemia and Sjogrens syndrome.  
CC This sequence represents a heavy chain CH2 domain-deleted huCC49  
CC polypeptide, used in the scope of the invention.

XX Sequence 362 AA;

Query Match 93.9%; Score 1762.5; DB 9; Length 362;

Best Local Similarity 92.5%; Pred. No. 3.3e-107;

Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPQORLEWIGYFSGNDDPKY 79

DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPQORLEWIGYFSGNDDPKY 60

QY 80 NERFKGKATLTADTASTAYVELSSLRSDTAVYFCTSLNWAYWGQGLTVTVSSASTKG 139  
 DB 61 NERFKGKATLTADTASTAYVELSSLRSDTAVYFCTSLNWAYWGQGLTVTVSSASTKG 120  
 QY 140 PSVFPLAPSSKSTSGTAAALCLVVDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSL 199  
 DB 121 PSVFPLAPSSKSTSGTAAALCLVVDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSL 180  
 QY 200 SSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCP----- 247  
 DB 181 SSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCP----- 240  
 QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
 DB 241 RCPAPGGSGGGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
 QY 293 QPENNYKTTTPVLDSDGSEFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTKQSLSP 352  
 DB 301 QPENNYKTTTPVLDSDGSEFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTKQSLSP 360  
 QY 353 GK 354  
 DB 361 GK 362  
 RESULT 6  
 ADW44587  
 ID ADW44587 standard; protein; 603 AA.  
 XX ADW44587;  
 AC ADW44587;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Antibody huCC49 heavy chain (CH2 domain deleted).  
 XX  
 XX Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;  
 KW Antiinflammatory; Gastrointestinal-Gen.; Dermatological; Antitumor;  
 KW Antirheumatic; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;  
 KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;  
 KW Vulnary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;  
 KW huCC49; Tag72; heavy chain variable region.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 PN WO2005000899-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 XX 28-JUN-2004; 2004WQ-US020945.  
 XX  
 PR 27-JUN-2003; 2003US-0483877P.  
 PR 03-OCT-2003; 2003US-0508810P.  
 PR 28-OCT-2003; 2003US-0515351P.  
 PR 30-OCT-2003; 2003US-0516030P.  
 XX  
 PA (BIOG-) BIOGEN IDEC MA INC.  
 XX  
 XX Glaser S, Reff M, Yang T, Wu X, Chinn P;  
 PI WPI; 2005-058133/06.  
 XX N-PSDB; ADW44584.  
 DR  
 XX  
 PT New composition comprising polypeptide dimers comprising at least four  
 PT binding sites and at least two polypeptide chains linked via at least one  
 PT interchain disulfide linkage, useful for treating e.g., cancer or  
 PT autoimmune diseases.  
 XX  
 XX Example 8; SEQ ID NO 19; 172pp; English.  
 PS  
 XX The invention relates to a composition comprising polypeptide dimers

CC comprising at least four binding sites and at least two polypeptide  
 CC chains, where the polypeptide chains comprise at least one heavy chain  
 CC portion and a synthetic connecting peptide, and where greater than about  
 CC 50% of the dimers comprise polypeptide chains that are linked via at  
 CC least one interchain disulfide linkage, or comprising minibody molecules  
 CC comprising two polypeptide chains, where the polypeptide chains comprise  
 CC a heavy chain portion and a synthetic connecting peptide, where the  
 CC polypeptide chains lack all or part of a CH2 domain, and where greater  
 CC than about 50% of the molecules are present in a form in which one of the  
 CC polypeptide chains are linked via at least one interchain disulfide  
 CC linkage. Also included are a nucleic acid molecule comprising a  
 CC nucleotide sequence encoding a polypeptide chain as defined above, a host  
 CC cell comprising a vector and a binding molecule comprising CH2 deleted  
 CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p388. The  
 CC synthetic connecting peptide comprises a (Gly-Ser)<sub>n</sub> linker attached to a  
 CC portion of a hinge region from IGG1, IGG3 or IGG4. The molecules are  
 CC bispecific and comprise at least one binding site specific for a soluble  
 CC ligand or for a cell surface molecule. The molecules comprise two binding  
 CC sites specific for a tumor cell antigen and two binding sites specific  
 CC for a prodrug. The synthetic connecting peptide comprises a proline  
 CC residue at position 243, Kabat numbering system. The synthetic connecting  
 CC peptide further comprises an alanine residue at position 244 and a  
 CC proline residue at position 245, Kabat numbering system. The polypeptide  
 CC dimers are tetraivalent minibody molecules. The composition is useful for  
 CC treating a subject that would benefit from treatment with an antigen  
 CC binding molecule, where the subject is suffering from cancer, lymphoma,  
 CC an autoimmune disease or disorder, or an inflammatory disease or disorder  
 CC The composition is useful for treating autoimmune diseases such as  
 CC Crohn's disease, inflammatory bowel disease, systemic lupus  
 CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's  
 CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,  
 CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious  
 CC anemia, Sjogren's syndrome, neurological disorders such as multiple  
 CC sclerosis, and inflammatory diseases or disorders such as cystic  
 CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The  
 CC polypeptide is useful for diagnostic or therapeutic purposes. The binding  
 CC molecules are also useful for pretargeting applications for  
 CC chemotherapeutic drug delivery. The present sequence represents a heavy  
 CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72  
 CC antibody huCC49.  
 XX  
 XX Sequence 603 AA;  
 SQ  
 Query Match 93.9%; Score 1762.5; DB 9; Length 603;  
 Best Local Similarity 97.1%; Pred. No. 5.8e-107;  
 Matches 334; Conservative 0; Mismatches 1; Indels 9; Gaps 1;  
 QY 20 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPORLEWIGYFSGNDDFKY 79  
 DB 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPORLEWIGYFSGNDDFKY 60  
 QY 80 NERFKGKATLTADTASTAYVELSSLRSDTAVYFCTSLNWAYWGQGLTVTVSSASTKG 139  
 DB 61 NERFKGKATLTADTASTAYVELSSLRSDTAVYFCTSLNWAYWGQGLTVTVSSASTKG 120  
 QY 140 PSVFPLAPSSKSTSGTAAALCLVVDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSL 199  
 DB 121 PSVFPLAPSSKSTSGTAAALCLVVDYFPEPTVSWNSGALTSVHTFPAVLQSSGLYSL 180  
 QY 200 SSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCP-----PGQP 250  
 DB 181 SSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCGSGSGGGGQP 240  
 QY 251 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 310  
 DB 241 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS 300  
 QY 311 FFYLSKLTVDKSRWQOGNVFSCVMHEALHNHYTKQSLSPGK 354  
 DB 301 FFYLSKLTVDKSRWQOGNVFSCVMHEALHNHYTKQSLSPGK 344  
 RESULT 7

ADW44588  
ID ADW44588 standard; protein; 621 AA.  
AC ADW44588;  
XX  
XX  
DT 24-MAR-2005 (first entry)  
XX  
XX Antibody huCC49 heavy chain (CH2 domain deleted/synthetic hinge).  
DE  
XX  
XX Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;  
KW Antinflammatory; Gastrointestinal-Gen.; Dermatological; Anticancer;  
KW Antirheumatic; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;  
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;  
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;  
KW huCC49; Tag72; heavy chain variable region.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 243..246  
FT /note= "Encoded by CCAGGA"  
XX  
XX WO2005000899-A2.  
XX  
XX 06-JAN-2005.  
XX  
XX 28-JUN-2004; 2004WO-US020945.  
XX  
XX 27-JUN-2003; 2003US-0483877P.  
PR 03-OCT-2003; 2003US-0508810P.  
PR 28-OCT-2003; 2003US-0515351P.  
PR 30-OCT-2003; 2003US-0516030P.  
XX  
XX (BIOG-) BIOGEN IDEC MA INC.  
XX  
XX Glaser S, Reff M, Yang T, Wu X, Chinn P;  
PI WPI; 2005-058133/06.  
DR N-PSDB; ADW44585.  
XX  
XX New composition comprising polypeptide dimers comprising at least four  
PT binding sites and at least two polypeptide chains linked via at least one  
PT interchain disulfide linkage, useful for treating e.g., cancer or  
PT autoimmune diseases.  
XX  
XX Claim 34; SEQ ID NO 20; 172pp; English.  
PS  
XX  
XX The invention relates to a composition comprising polypeptide dimers  
CC comprising at least four binding sites and at least two polypeptide  
CC chains, where the polypeptide chains comprise at least one heavy chain  
CC portion and a synthetic connecting peptide, and where greater than about  
CC 50% of the dimers comprise polypeptide chains that are linked via at  
CC least one interchain disulfide linkage, or comprising minibody molecules  
CC comprising two polypeptide chains, where the polypeptide chains comprise  
CC a heavy chain portion and a synthetic connecting peptide, where the  
CC polypeptide chains lack all or part of a CH2 domain, and where greater  
CC than about 50% of the molecules are present in a form in which one of the  
CC polypeptide chains are linked via at least one interchain disulfide  
CC linkage. Also included are a nucleic acid molecule comprising a  
CC nucleotide sequence encoding a polypeptide chain as defined above, a host  
CC cell comprising a vector and a binding molecule comprising CH2 deleted  
CC heavy and light chains of the antibodies huCC49 and PRIMATIZED p3E8. The  
CC synthetic connecting peptide comprises a (Gly-Ser)<sup>n</sup> linker attached to a  
CC portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are  
CC bispecific and comprise at least one binding site specific for a soluble  
CC ligand or for a cell surface molecule. The molecules comprise two binding  
CC sites specific for a tumor cell antigen and two binding sites specific  
CC for a prodrug. The synthetic connecting peptide comprises a proline  
CC residue at position 243, Kabat numbering system. The synthetic connecting  
CC peptide further comprises an alanine residue at position 244 and a

CC proline residue at position 245, Kabat numbering system. The polypeptide  
CC dimers are tetraivalent minibody molecules. The composition is useful for  
CC treating a subject that would benefit from treatment with an antigen  
CC binding molecule, where the subject is suffering from cancer, lymphoma,  
CC an autoimmune disease or disorder, or an inflammatory disease or disorder  
CC The composition is useful for treating autoimmune diseases such as  
CC Crohn's disease, inflammatory bowel disease, systemic lupus  
CC erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's  
CC syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,  
CC myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious  
CC anemia, Sjogren's syndrome, neurological disorders such as multiple  
CC sclerosis, and inflammatory diseases or disorders such as cystic  
CC fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The  
CC polypeptide is useful for diagnostic or therapeutic purposes. The binding  
CC molecules are also useful for pretargeting applications for  
CC chemotherapeutic drug delivery. The present sequence represents a heavy  
CC chain variable region (optionally CH2 domain deleted) from the anti-Tag72  
CC antibody huCC49.  
XX  
XX Sequence 621 AA;  
SQ  
Query Match 93.9%; Score 1762.5; DB 9; Length 621;  
Best Local Similarity 92.5%; Pred. No. 6e-107;  
Matches 335; Conservative 0; Mismatches 0; Indels 27; Gaps 1;  
QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVVKQNPQRLEWIGYRSPGNDPKY 79  
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAIHVVKQNPQRLEWIGYRSPGNDPKY 60  
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDITAVYFCTSLNMAWVGQGLTVTVSSASTKG 139  
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDITAVYFCTSLNMAWVGQGLTVTVSSASTKG 120  
QY 140 PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 199  
DB 121 PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 180  
QY 200 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPCP----- 247  
DB 181 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPEKSCDTPPCP 240  
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 292  
DB 241 RCPAPGGSSGGSGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG 300  
QY 293 QPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 352  
DB 301 QPENNYKTPPVLDSDGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 360  
QY 353 GK 354  
DB 361 GK 362  
RESULT 8  
ID ADW77053 standard; protein; 362 AA.  
AC ADW77053;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Heavy chain CH2 domain-deleted huCC49 polypeptide #4.  
DE  
XX Protein production; protein purification; cancer; lymphoma;  
KW autoimmune disease; inflammation; Crohns disease;  
KW inflammatory bowel disease; systemic lupus erythematosus;  
KW ulcerative colitis; rheumatoid arthritis; Goodpasture's syndrome;  
KW Grave's disease; Hashimoto's disease; pemphigus vulgaris;  
KW myasthenia gravis; scleroderma; autoimmune hemolytic anemia;  
KW pernicious anemia; Sjogrens syndrome; immunosuppressive; antianemic;  
KW dermatological; muscular-gen.; neuroprotective; thyromimetic;  
KW antithyroid; nephrotropic; antirheumatic; antiarthritic;





CC prolonging the survival time of tumour-bearing animals and for treating  
CC tumours. The present sequence is human CH2 domain deleted C2B8 protein.  
CC This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 360 AA;  
Query Match 89.7%; Score 1683; DB 5; Length 360;  
Best Local Similarity 88.6%; Pred. No. 5.2e-102;  
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;  
QY 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQTP 60  
QY 61 GQRLWIGYFPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDYAVYFCTRSIN 120  
DB 61 GRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTY 120  
QY 121 MA-----YWGCGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 174  
DB 121 YGGDWYFNVWGAGTITVTSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 180  
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP 240  
QY 235 KSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 KSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300  
QY 295 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 360  
RESULT 10  
ABB2833  
ID ABB2833 standard; protein; 360 AA.  
XX  
AC ABB2833;  
XX  
XX 31-MAR-2003 (first entry)  
XX  
DE Antibody C2B8 CH2 domain deleted heavy chain.  
XX  
KW C2B8; antibody; cytostatic; antiallergic; antianemic; antiaschmatic;  
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
KW thymometric; hepatotropic; haemostatic; antileprotic; antibacterial;  
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
KW dermatological; immunosuppressive; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX WO200296948-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002374.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
PR 21-DEC-2001; 2001US-0341858P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;  
XX  
XX WPI; 2003-140446/13.  
DR N-PSDB; AB224017.  
XX  
XX Novel dimeric antibody useful for treating immune disorder and neoplastic  
XX disorder, has several non-covalently associated monomeric subunits.  
PT  
PT  
XX

PS Example 1; Fig 1B; 78pp; English.  
XX  
CC The invention relates to a dimeric antibody (I) comprising several  
CC monomeric subunits, where the monomeric subunits are non-covalently  
CC associated. (I) is useful for treating a disorder, especially immune  
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a  
CC detailed description of the various uses of (I)). The present sequence  
CC represents the antibody C2B8 CH2 domain deleted heavy chain  
XX  
SQ Sequence 360 AA;  
Query Match 89.7%; Score 1683; DB 6; Length 360;  
Best Local Similarity 88.6%; Pred. No. 5.2e-102;  
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;  
QY 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQTP 60  
QY 61 GQRLWIGYFPGNDDFKYNRFKPKATLTADTSASTAYVELSSLRSEDYAVYFCTRSIN 120  
DB 61 GRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTY 120  
QY 121 MA-----YWGCGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 174  
DB 121 YGGDWYFNVWGAGTITVTSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 180  
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEP 240  
QY 235 KSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294  
DB 241 KSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300  
QY 295 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 354  
DB 301 ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 360  
RESULT 11  
AAE27923  
ID AAE27923 standard; protein; 470 AA.  
XX  
AC AAE27923;  
XX  
XX 27-DEC-2002 (first entry)  
XX  
XX Human C2B8 antibody heavy chain protein.  
XX  
XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.  
XX  
XX Homo sapiens.  
XX  
XX WO200260955-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002373.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
PR 16-NOV-2001; 2001US-0331481P.  
PR

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XX (IDEC-) IDEC PHARM CORP.
XX Braslawsky GR, Hanna N, Chinn P;
XX WPI; 2002-698547/75.
XX N-PSDB; AAD45752.
XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
XX -72, or C2B8 antibody reactive with CD20, useful for treating
XX myelosuppressed patient suffering from a neoplastic disorder.
XX Example 1; Fig 1A; 74pp; English.
XX
XX The present invention relates to domain deleted CC49 or C2B8 antibodies.
XX Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
XX deleted sequence in which CH2 domain has been deleted and are reactive
XX with tumor associated antigen (TAG)-72. The C2B8 antibodies are reactive
XX with CD20 and comprise a heavy chain having a sequence of a derived
XX domain deleted C2B8 construct where the CH2 domain has been deleted.
XX Sequences of the invention are useful for imaging a neoplasm. They are
XX also useful for treating myelosuppressed patients suffering from
XX neoplastic disorder such as haematologic neoplasm, preferably non-
XX Hodgkin's lymphoma. Antibodies of the invention are also used to treat
XX neoplastic disorder, colon cancer and haematologic malignancy. They are
XX useful for reducing tumour size, inhibiting tumour growth and/or
XX prolonging the survival time of tumour-bearing animals and for treating
XX tumours. The present sequence is human C2B8 heavy chain protein. This
XX sequence is used in the exemplification of the invention
XX
XX Query Match 86.0%; Score 1614; DB 5; Length 470;
XX Best Local Similarity 67.7%; Pred. No. 2.3e-97;
XX Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;
XX
QY 1 MGSLILLFVAVATRVLSQVLVQSGAEVVKPGASVKSCKASGYTFTDTHAIHWKQNP 60
Db 1 MGSLILLFVAVATRVLSQVLVQSGAEVVKPGASVKSCKASGYTFTSYNNHVKQTP 60
QY 61 GQPLEWIGVSPGNDPKYNERPKGKATLTADTSASTAYVLSLSSEDTAVVFCRSLN 120
Db 61 GRGLEWIGALYPGNGDTSYNGKPKGKATLTADKSSSTAYVQLSSLTSEDSAVYICARSTY 120
QY 121 MA-----YVGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYPPEPTVVS 174
Db 121 YGQDWTFNVWGAGTTTVTSASATKGPSVFPFLAPSSKSTSGTAAALGCLVKDYPPEPTVVS 180
QY 175 WNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSPSSLTGTQYICNVNHKPSNTKVDKKVEP 234
Db 181 WNSGALTSGVHTTFAVLQSSGLYSLSSVTVTPSPSSLTGTQYICNVNHKPSNTKVDKKAEP 240
QY 235 KSCDKTHCTCPCP----- 247
Db 241 KSCDKTHCTCPCPAPELLGGPSVFLPPKPKOTLMTISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
Db 301 YVDGVEVHNKATPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTIS 360
QY 248 ---GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
Db 361 KAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
QY 305 LDSGGSFFLYSKLTVDKSRWQQGNVPCSVNHEALHNNHYTKSLSPGK 354
Db 421 LDSGGSFFLYSKLTVDKSRWQQGNVPCSVNHEALHNNHYTKSLSPGK 470
XX
RESULT 12
ABB82832
ID ABB82832 standard; protein; 470 AA.
XX
```

```
AC ABB82832;
XX 31-MAR-2003 (first entry)
XX Antibody C2B8 heavy chain.
XX
XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
XX vsotropic; immunomodulator; prozoacide; antidiabetic; nephrotropic;
XX thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
XX neuroprotective; antipsoptic; antirheumatic; antiarthritic; antitumor;
XX dermatological; immunosuppressive; antiinflammatory.
XX
XX Homo sapiens.
XX
XX WO200296948-A2.
XX 05-DEC-2002.
XX
XX 29-JAN-2002; 2002WO-US002374.
XX
XX 29-JAN-2001; 2001US-0264318P.
XX 16-NOV-2001; 2001US-0331481P.
XX 21-DEC-2001; 2001US-0341858P.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX WPI; 2003-140446/13.
XX N-PSDB; AB224016.
XX
XX Novel dimeric antibody useful for treating immune disorder and neoplastic
XX disorder, has several non-covalently associated monomeric subunits.
XX Example 1; Fig 1A; 78pp; English.
XX
XX The invention relates to a dimeric antibody (I) comprising several
XX monomeric subunits, where the monomeric subunits are non-covalently
XX associated. (I) is useful for treating a disorder, especially immune
XX disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
XX resistant Hodgkin's disease high grade, low grade and intermediate grade
XX non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
XX lymphoplasmacytoid lymphoma (LP), mantle cell lymphoma (MCL), follicular
XX lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
XX AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
XX lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
XX diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
XX small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
XX cleaved and large cell lymphomas, in a mammal. (I) is also useful for
XX treating allergic rhinitis, autoimmune haemolytic anemia, allergic
XX contact dermatitis, Addison's disease, atopic dermatitis, amyloidosis,
XX aplastic anemia, arteritis, asthma, ataxia-telangiectasia, autoimmune
XX oophoritis, Burger's disease, bronchitis, candidiasis, Post-myocardial
XX infarction syndrome, carditis, celiac sprue, Chagas's disease, Chediak-
XX Higashi syndrome, Crohn's disease, cryoglobulinemia, diabetes mellitus,
XX erythema multiforme, glomerulonephritis, Goodpasture's syndrome, Grave's
XX disease, Hashimoto's thyroiditis, haemolytic disease of the newborn,
XX hepatitis, idiopathic thrombocytopenic purpura, leprosy, Lyme disease,
XX multiple sclerosis, myasthenia gravis, polymyositis, scleroderma,
XX paroxysmal nocturnal haemoglobinuria, psoriasis, Raynaud's phenomenon/
XX syndrome, rheumatoid arthritis, Sjogren's syndrome, systemic lupus
XX erythematosus, transplant rejection, and ulcerative colitis. (I) is also
XX useful for inducing hyper-cross-linking of membrane antigens, for killing
XX or inhibiting selected cell populations in the treatment of diseases such
XX as cancer and immune disorders, for treating myelosuppressed or
XX myelocompromised patients, for inducing apoptosis in the target cell
XX population or effectively block cell surface receptors necessary for the
XX growth of neoplastic cells, in viral or bacterial neutralization, for
XX diagnostic imaging of tumours, and for reducing tumour size, inhibiting
XX tumour growth and/or prolonging the survival time of tumour-bearing
XX animals. The present sequence represents the antibody C2B8 heavy chain
XX
XX Sequence 470 AA;
```

Query Match 86.0%; Score 1614; DB 6; Length 470;  
Best Local Similarity 67.7%; Pred. No. 2.3e-97;  
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;  
QY 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTSYNHWKQTP 60  
QY 61 GQRLWIGYFPGNDDFKYNRPFKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWIGAIYFGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTY 120  
QY 121 MA-----YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTS 174  
DB 121 YGGDWYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180  
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEP 234  
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEP 240  
QY 235 KSCDKHTCTPPCP----- 247  
DB 241 KSCDKHTCTPPCPAPPELLGGPSVFLPCKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
QY 248 ----- 247  
DB 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304  
DB 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
QY 305 LPSDGSFFLYSKLTVDKSRWQGNVFSQVSCVMHEALHNYHTQKSLSLSPGK 354  
DB 421 LPSDGSFFLYSKLTVDKSRWQGNVFSQVSCVMHEALHNYHTQKSLSLSPGK 470  
RESULT 13  
AAMS2156  
ID AAMS2156 standard; protein; 731 AA.  
AC AAMS2156;  
XX  
XX  
DT 05-FEB-2002 (first entry)  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
XX 26-MAR-2001; 2001WO-GB001324.  
XX  
PR 03-APR-2000; 2000GB-00008049.  
PR 02-OCT-2000; 2000US-0237159P.  
XX  
XX (ANTI-) ANTISOMA RES LTD.  
XX PA  
XX PA  
XX Young RJ;  
XX  
XX WPI; 2001-662969/76.  
XX  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.

XX Claim 20; Fig 7; 176pp; English.  
PS The invention relates to a compound which comprises a target cell-  
XX specific portion, comprising a humanised monoclonal antibody, having  
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding  
CC fragment and a cytotoxic portion having endonucleolytic activity.  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02738. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis  
XX  
SQ Sequence 731 AA;  
Query Match 86.0%; Score 1613.5; DB 4; Length 731;  
Best Local Similarity 67.7%; Pred. No. 4e-97;  
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;  
QY 1 MGWSLILFLVAVATRVLSQVLQVSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60  
DB 1 MGWSLILFLVATATGVHSQVLQVSGAEVVKPGASVKISCKASGYTFSAYWVQAP 60  
QY 61 GQRLWIGYFPGNDDFKYNRPFKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLN 120  
DB 61 GRGLEWVGELLPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSSLRSEDYAVYCARSYD 120  
QY 121 ---MAYWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177  
DB 121 FAWFAYWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180  
QY 178 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSC 237  
DB 181 GALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSC 240  
QY 238 DKHTCTPPCP----- 247  
DB 241 DKHTCTPPCPAPPELLGGPSVFLPCKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300  
QY 248 ----- 247  
DB 301 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360  
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307  
DB 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420  
QY 308 DGSFFLYSKLTVDKSRWQGNVFSQVSCVMHEALHNYHTQKSLSLSPGK 354  
DB 421 DGSFFLYSKLTVDKSRWQGNVFSQVSCVMHEALHNYHTQKSLSLSPGK 467  
RESULT 14  
AAMS2159  
ID AAMS2159 standard; protein; 741 AA.  
XX  
XX AAMS2159;  
XX  
XX 05-FEB-2002 (first entry)  
XX  
XX Humanised HMFG-1 heavy chain/DNase I fusion protein 4.  
XX  
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200174905-A1.  
XX  
XX 11-OCT-2001.  
XX  
XX 26-MAR-2001; 2001WO-GB001324.  
XX  
XX 03-APR-2000; 2000GB-00008049.  
XX  
XX (ANTI-) ANTISOMA RES LTD.  
XX PA  
XX PA  
XX Young RJ;  
XX  
XX WPI; 2001-662969/76.  
XX  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.

PR 02-OCT-2000; 2000US-0237159P.  
XX (ANTI-) ANTISOMA RES LTD.  
XX  
XX Young RJ;  
XX WPI; 2001-662969/76.  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanized monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity.  
XX  
XX Claim 20; Fig 10; 176pp; English.  
PS  
CC The invention relates to a compound which comprises a target cell-  
CC specific portion, comprising a humanised monoclonal antibody, having  
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding  
CC fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis  
XX  
XX Sequence 741 AA;  
SQ  
Query Match 86.0%; Score 1613.5; DB 4; Length 741;  
Best Local Similarity 67.7%; Pred. No. 4.1e-97;  
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;  
QY 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTDTHAIHWKQP 60  
DB 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTDTHAIHWKQP 60  
QY 61 GORLEWIGVSPGNDKYNRFKATLTADTSASTAYVELLSRSDTAVYFCTSLN 120  
DB 61 GORLEWIGVSPGNDKYNRFKATLTADTSASTAYVELLSRSDTAVYFCTSLN 120  
QY 121 ---MAYWQGGTLVTVSSASTKGPSVFLPAPSKSTSGGTAAALGCLVVDYFPEPVTVS 177  
DB 121 FAWPAYWGGTLVTVSSASTKGPSVFLPAPSKSTSGGTAAALGCLVVDYFPEPVTVS 180  
QY 178 GALTSGVTFPAVLQSSGLYSLSSVTVPPSSSLGHTQVTCNVNHPKSNKVDKVEPKSC 237  
DB 181 GALTSGVTFPAVLQSSGLYSLSSVTVPPSSSLGHTQVTCNVNHPKSNKVDKVEPKSC 240  
QY 238 DKTHCTPCPCP----- 247  
DB 241 DKTHCTPCPCPAPPELLGGSVFLFPKPKDITLMSRTPEVTVVDVSHEDPEVKFNWYVD 300  
QY 248 ----- 247  
DB 301 GVEVHNKTKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360  
QY 248 GQPREPQVYTLPPSDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307  
DB 361 GQPREPQVYTLPPSDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420  
QY 308 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 354  
DB 421 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467  
RESULT 15  
AAB08026  
ID AAB08026 standard; protein; 470 AA.  
XX AAB08026;  
XX  
XX 12-SEP-2003 (revised)  
DT 14-NOV-2000 (first entry)  
XX  
XX A dimeric anti-CD20 heavy chain polypeptide.

KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;  
KW complement system; Fc gamma receptor; cytotoxic effector cell;  
KW host immune cell; programmed cell death; allergic disorder; cancer;  
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;  
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;  
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;  
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;  
KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;  
KW diabetes mellitus; candidiasis; aplastic anaemia.  
XX Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "signal peptide"  
FT Protein 20..140  
FT /note= "murine anti-human CD20 heavy chain variable  
FT region"  
FT Protein 141..470  
FT /note= "human gamma 1 heavy chain constant region"  
XX  
FN WO200044788-A1.  
XX  
XX 03-AUG-2000.  
XX 28-JAN-2000; 2000WO-US001893.  
XX 28-JAN-1999; 98US-00238741.  
PA (IDEC-) IDEC PHARM CORP.  
PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;  
DR WPI; 2000-514811/46.  
DR N-PSDB; AAA63531.  
XX  
XX Genetically engineering immunoglobulin (Ig) G/IgG dimers for the  
treatment of cancers, allergic disorders and autoimmune conditions.  
XX  
XX Example 1; Fig 2A-C; 65pp; English.  
PS The present sequence represents a dimeric anti-CD20 light chain  
CC polypeptide. The dimeric immunoglobulin is used in the method of an  
CC invention. The specification describes a method for producing an  
CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically  
CC engineering a monoclonal antibody to introduce a cysteine molecule which  
CC inhibits formation of intramolecular disulphide bridges between sister  
CC heavy chains on the same antibody molecule. The dimer is a homodimer or  
CC heterodimer that is capable of activating components of the complement  
CC system, and has the ability to activate and kill cells via the complement  
CC cascade. The dimer is also capable of binding to Fc gamma receptors on  
CC cytotoxic effector cells and on host immune cells, and is capable of  
CC initiating programmed cell death. The IgG/IgG dimers may be used to treat  
CC allergic disorders, cancers and autoimmune diseases such as allergic  
CC asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis,  
CC atopic dermatitis, Crohn's disease, Graves's disease, food allergies,  
CC allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They  
CC may also be used to treat a range of other diseases and disorders such as  
CC rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's  
CC disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis  
CC and aplastic anaemia. They are also useful for inducing hyper-cross-  
CC linking of membrane antigens and for the preferential killing of selected  
CC cell populations. (Updated on 12-SEP-2003 to standardise OS field)  
XX  
XX Sequence 470 AA;  
SQ  
Query Match 86.0%; Score 1613; DB 3; Length 470;  
Best Local Similarity 67.7%; Pred. No. 2.7e-97;  
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;  
QY 1 MGWSLILFLVANATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTDTHAIHWKQP 60

```
Db      1  MWNSLIILFLVAVATRVLSQVLOQPQGAELVKPGASVKMSCKASGYTFTSYNMHWKQTP 60
Qy      61  GORLEWIGYFSPGNDDFKYNERFKGKATLTADTSASTAYVELSSLRSEDTAIFYCTRSLN 120
Db      61  GRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTY 120
Qy     121  MA-----YWGQGLTVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 174
Db     121  YGGDWYFNWVGAGTTVTVAASATKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Qy     175  WNSGALTSVHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHRKPSNTKVDKKVEP 234
Db     181  WNSGALTSVHTFPAVLQSSGLYSLSVVTVFPSSSLGTQTYICNVNHRKPSNTKVDKKVEP 240
Qy     235  KSCDKTHTCPPCP----- 247
Db     241  KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy     248  ----- 247
Db     301  YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Qy     248  ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 304
Db     361  KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 420
Qy     305  LDSGSPFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 354
Db     421  LDSGSPFLYSKLTVDKSRWQQGNVFCFSCVMHEALHNYHTQKSLSLSPGK 470
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Search completed: February 16, 2006, 10:17:39  
Job time : 197.879 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 10:38:47 ; Search time 92.5253 Seconds  
(without alignments)  
1083.802 Million cell updates/sec

Title: US-10-058-069-9

Perfect score: 1243

Sequence: 1 MDSQAQVLMMLLLWVGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	93.8	240	3	US-09-301-593-28 Sequence 28, Appl
2	1166	93.8	240	4	US-10-159-006-28 Sequence 28, Appl
3	1140	91.7	220	5	US-10-880-028-19 Sequence 19, Appl
4	1140	91.7	220	5	US-10-880-320-19 Sequence 19, Appl
5	1136	91.4	240	3	US-09-301-593-36 Sequence 36, Appl
6	1136	91.4	240	4	US-10-159-006-36 Sequence 36, Appl
7	1135	91.3	220	5	US-10-880-028-27 Sequence 27, Appl
8	1135	91.3	220	5	US-10-880-320-27 Sequence 27, Appl
9	1125.5	90.5	239	6	US-10-723-003-14 Sequence 14, Appl
10	1125.5	90.5	239	6	US-11-004-639-14 Sequence 14, Appl
11	1125	90.5	240	3	US-09-799-514-8 Sequence 8, Appl
12	1122	90.3	240	4	US-10-630-406-8 Sequence 8, Appl
13	1122	90.3	240	6	US-11-073-453-8 Sequence 8, Appl
14	1121.5	90.2	239	3	US-09-249-011A-22 Sequence 22, Appl
15	1119.5	90.1	241	6	US-11-031-485-62 Sequence 62, Appl
16	1115	89.7	240	5	US-10-938-353-24 Sequence 24, Appl
17	1105.5	88.9	241	6	US-11-031-485-24 Sequence 24, Appl
18	1082	87.0	220	5	US-10-644-277-20 Sequence 20, Appl
19	1070	86.1	220	3	US-09-301-593-17 Sequence 17, Appl
20	1070	86.1	220	4	US-10-159-006-17 Sequence 17, Appl
21	1064	85.6	220	3	US-09-995-693-1 Sequence 1, Appl
22	1064	85.6	220	4	US-10-232-408-1 Sequence 1, Appl
23	1064	85.6	220	5	US-10-644-277-92 Sequence 92, Appl
24	1064	85.6	238	6	US-11-013-537-1 Sequence 1, Appl
25	1063	85.5	220	5	US-10-644-277-40 Sequence 40, Appl
26	1059	85.2	220	5	US-10-644-277-68 Sequence 68, Appl
27	1054	84.8	220	5	US-10-644-277-4 Sequence 4, Appl

28	1047	84.2	239	3	US-09-825-013-9	Sequence 9, Appl
29	1044	84.0	242	3	US-09-819-266-26	Sequence 26, Appl
30	1040	83.7	238	4	US-10-171-452A-38	Sequence 38, Appl
31	1040	83.7	238	4	US-10-171-452A-56	Sequence 56, Appl
32	1040	83.7	238	4	US-10-353-708-38	Sequence 38, Appl
33	1040	83.7	238	4	US-10-353-708-56	Sequence 56, Appl
34	1040	83.7	238	4	US-10-731-984-3	Sequence 3, Appl
35	1040	83.7	238	4	US-10-731-984-27	Sequence 27, Appl
36	1030	82.9	238	4	US-10-171-452A-44	Sequence 44, Appl
37	1030	82.9	238	4	US-10-171-452A-50	Sequence 50, Appl
38	1030	82.9	238	4	US-10-353-708-44	Sequence 44, Appl
39	1030	82.9	238	4	US-10-353-708-50	Sequence 50, Appl
40	1030	82.9	238	4	US-10-731-984-11	Sequence 11, Appl
41	1030	82.9	238	4	US-10-731-984-19	Sequence 19, Appl
42	1016.5	81.8	241	5	US-10-723-003-22	Sequence 22, Appl
43	1016.5	81.8	241	6	US-11-004-639-22	Sequence 22, Appl
44	1014.5	81.6	238	4	US-10-467-253-14	Sequence 14, Appl
45	1010.5	81.3	235	5	US-10-938-353-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-301-593-28

; Sequence 28, Application US/09301593A

; Publication No. US20020052480A1

; GENERAL INFORMATION:

; APPLICANT: Park, John E.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leiger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890001

; CURRENT APPLICATION NUMBER: US/09/301,593A

; CURRENT FILING DATE: 1999-04-29

; EARLIER APPLICATION NUMBER: EP 98107925.4

; EARLIER FILING DATE: 1998-04-30

; EARLIER APPLICATION NUMBER: US 60/086,049

; EARLIER FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-301-593-28

Query Match 93.8%; Score 1166; DB 3; Length 240;

Best Local Similarity 93.3%; Pred. No. 1.7e-64;

Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDSQAQVLMMLLLWVGTCGDIIVMSQSPSLAVSLGERTVLTNCKSSQSLLYSNQKNYLA 60

Db 1 MDSQAQVLMMLPLWVGTCGDIIVMSQSPSLAVSVGKVTMSCKSSQSLLYSNQKNYLA 60

QY 61 WYQOKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQVYSY 120

Db 61 WYQOKPGQSPKLLIFWASTRESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCCQVYSY 120

QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180

Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180

QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2

US-10-159-006-28

```
; Sequence 28, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: Fc $\alpha$ -specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-159-006-28

Query Match          93.8%; Score 1166; DB 4; Length 240;
Best Local Similarity 93.3%; Pred. No. 1.7e-64;
Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDSQAQVLLMLLWVSGTGGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60
DB 1 MDSQAQVLLMLLWVSGTGGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLA 60
QY 61 WYQKFGQSPKLLIYWASARESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSY 120
DB 61 WYQKFGQSPKLLIFWASTRESGVPRFTGSGGTFDNLTIISSVQAEADVAVVYCCQYFSY 120
QY 121 PLTFGAGTKLELKRVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 121 PLTFGAGTKLELKRVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
QY 181 QSGNSQESVTEQSKDSTVSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 181 QSGNSQESVTEQSKDSTVSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240

RESULT 3
US-10-880-028-19
; Sequence 19, Application US/10880028
; Publication No. US20050163782A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; TITLE OF INVENTION: OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,028
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-10-880-320-19

Query Match          91.7%; Score 1140; DB 5; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.3e-63;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQKFGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQKFGQSPKLLIYWASAR 60
QY 81 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRVAAPS 140
DB 61 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRVAAPS 120
QY 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQSKDSTYS 200
DB 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQSKDSTYS 180
QY 201 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220

RESULT 4
US-10-880-320-19
; Sequence 19, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Tzung-Horng
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; TITLE OF INVENTION: OF BINDING POLYPEPTIDES
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; US-10-880-320-19

Query Match          91.7%; Score 1140; DB 5; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.3e-63;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQKFGQSPKLLIYWASAR 80
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQKFGQSPKLLIYWASAR 60
QY 81 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRVAAPS 140
DB 61 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKRVAAPS 120
```





```
Db 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 60
QY 81 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYISYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYISYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 200
Db 121 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 240
Db 181 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 220
```

RESULT 8

```
US-10-880-320-27
; Sequence 27, Application US/10880320
; Publication No. US20050163783A1
; GENERAL INFORMATION:
; APPLICANT: BRASLAWKY, Gary R.
; APPLICANT: GLASER, Scott
; APPLICANT: YANG, Izung-Hornig
; APPLICANT: HOPP, Jennifer
; APPLICANT: CHINN, Paul
; TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
; FILE REFERENCE: IDV-001
; CURRENT APPLICATION NUMBER: US/10/880,320
; CURRENT FILING DATE: 2004-06-28
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/483877
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/508810
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/515351
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/516030
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-880-320-27
```

```
Query Match 91.3%; Score 1135; DB 5; Length 220;
Best Local Similarity 99.5%; Pred. No. 1.3e-62;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 80
Db 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQPKLLIYWASAR 60
QY 81 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYISYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYISYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 200
Db 121 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYTS 180
QY 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 240
Db 181 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 220
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RESULT 9

```
US-10-723-003-14
; Sequence 14, Application US/10723003
```

```
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14
```

```
Query Match 90.5%; Score 1125.5; DB 5; Length 239;
Best Local Similarity 89.6%; Pred. No. 5.3e-62;
Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDSQAQVLMLELLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYL 60
Db 1 MESQTQVFLSLLWVSGTCGNIWMTQSPSSLAVSAGEKVTMTSCKSSQSLVYSSNQKYL 60
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYIS 120
Db 61 WYQKPGQSPKLLIYWASTRESGVDPDRFSGSGSGDFTLTSSVQAEADVAVVYCOQYIS 119
QY 121 PLTFCAGTKLEKRTVAAPSVFIPPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNAL 180
Db 120 SYTFGGGFKLEKRTVAAPSVFIPPPSDEQLKSGTASVVCLNNFYPREAKVQWVDNAL 179
QY 181 QSGNSQESVTEQDSKDYTSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 240
Db 180 QSGNSQESVTEQDSKDYTSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239
```

RESULT 10

```
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14
```

Query Match 90.5%; Score 1125.5; DB 6; Length 239;

```
Best Local Similarity 89.6%; Pred. No. 5.3e-62;
Matches 215; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MDSQAQVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 60
Db 1 MESQTVFLSLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 60

Qy 61 WYQKQSPKLLIYWASARESGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSY 120
Db 61 WYQKQSPKLLIYWASTRESGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCHQYFS- 119

Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180
Db 120 SYTFGGGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 179

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 180 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11
US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar
; FILE REFERENCE: PT015P1
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-8

Query Match 90.5%; Score 1125; DB 3; Length 240;
Best Local Similarity 90.3%; Pred. No. 5.7e-62;
Matches 214; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 4 QAQVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 63
Db 4 QTVQFISLLLVWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQTVLYSSDNKNYLA 63

Qy 64 QKPGQSPKLLIYWASARESGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSYPLT 123
Db 64 QKPGQSPKLLIYWASTRESGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSYTPS 123

Qy 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 183
Db 124 FGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSG 183

Qy 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 184 NSQESVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240

RESULT 12
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
```

```
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

Query Match 90.3%; Score 1122; DB 4; Length 240;
Best Local Similarity 90.0%; Pred. No. 8.8e-62;
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDSQAQVLMLLLVWVSGTCGDIWMSQSPDSLAVSLGSRVTLNCKSSOSLLYSGNQKNYLA 60
Db 1 MEAPQALLFLLLVWLPDPTGDIWMTQSPDSLAVSLGERATINCKSSOSLLSSGNQKNYLA 60

Qy 61 WYQKQSPKLLIYWASARESGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCCQYYSY 120
Db 61 WYQKQSPKLLIYASTRQSGVDPFRFSGSGGTDTLTITSSVQAEADVAVYCYDQRY 120

Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180
Db 121 PFTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL 180

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240

RESULT 13
US-11-073-453-8
; Sequence 8, Application US/11073453
; Publication No. US20050202022A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/11/073,453
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-073-453-8

Query Match 90.3%; Score 1122; DB 6; Length 240;
Best Local Similarity 90.0%; Pred. No. 8.8e-62;
Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
```

```
QY 1 MDSQAQVLM LLLLVSGTCGDIYMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 MEAPAQLFL LLLLVLPDTTGDIYVMTQSPDSLAVSLGERATINCKSSQSLLYSGNQKNYLA 60
QY 61 WYQOKPGQPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCQYYSY 120
Db 61 WYQOKPGQPKLLIYVASTRQSGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCQYDRY 120
QY 121 PLTFGAGTKLELKRVTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 121 PTFGQGTKEIKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
QY 181 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 14
US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US2002017685A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702-0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22
```

```
Query Match 90.2%; Score 1121.5; DB 3; Length 239;
Best Local Similarity 90.4%; Pred. No. 9.4e-62;
Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDSQAQVLM LLLLVSGTCGDIYMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 MDSQAQVLI LLLLVSGTCGDIYVMTQSPDSLAVSLGERATISCKSSQSLLYSGNRTRENYLA 60
QY 61 WYQOKPGQPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCQYYSY 120
Db 61 WYQOKPGQPKLLIYVASTRQSGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCQSYNL 120
QY 121 PLTFGAGTKLELKRVTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 121 -YTFGQGTKEIKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 179
QY 181 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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RESULT 15
US-11-031-485-62
; Sequence 62, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: FULLER, NICHOLAS
```

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; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MadCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 62
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-62

Query Match 90.1%; Score 1119.5; DB 6; Length 241;
Best Local Similarity 90.3%; Pred. No. 1.3e-61;
Matches 215; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 4 QAQVLM LLLLVSGTCGDIYMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 63
Db 4 QTQVFIS LLLLVSGTGDIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLA 63
QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYVCQYYSY-PL 122
Db 64 QKPGQSPKLLIYWASIREYGVDPDRFSGSGSGTDFTLTISSVQAEADVAVYFCQYYSIPPL 123
QY 123 TFGAGTKLELKRVTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 182
Db 124 TFGGQTKVEIKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 183
QY 183 GNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 184 GNSQESVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

Search completed: February 16, 2006, 10:43:11
Job time : 93.5253 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 10:39:32 ; Search time 8.88889 Seconds  
(without alignments)  
383.795 Million cell updates/sec

Title: US-10-058-069-9

Perfect score: 1243

Sequence: 1 MDSQAQVLMILLWVGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US03\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043.5	84.0	666	6	US-10-981-356A-29
2	1043.5	84.0	667	7	US-11-096-046-29
3	1040	83.7	238	7	US-11-158-505-1
4	1040	83.7	238	7	US-11-158-505-3
5	1040	83.7	238	7	US-11-158-505-25
6	1040	83.7	238	7	US-11-158-505-27
7	1030	82.9	238	7	US-11-158-505-9
8	1030	82.9	238	7	US-11-158-505-11
9	1030	82.9	238	7	US-11-158-505-17
10	1030	82.9	238	7	US-11-158-505-19
11	1030	82.9	238	7	US-11-158-505-74
12	1000.5	80.5	666	6	US-10-981-356A-25
13	1000.5	80.5	666	6	US-10-981-356A-27
14	1000.5	80.5	666	6	US-10-981-356A-28
15	1000.5	80.5	666	7	US-11-096-046-27
16	1000.5	80.5	667	7	US-11-096-046-25
17	1000.5	80.5	667	7	US-11-096-046-28
18	1000.5	80.5	692	6	US-10-981-356A-26
19	1000.5	80.5	695	7	US-11-096-046-26
20	994.5	80.0	235	7	US-11-128-900-14
21	994.5	80.0	235	7	US-11-128-900-65
22	992	79.8	218	7	US-11-158-505-4
23	992	79.8	218	7	US-11-158-505-28
24	991.5	79.8	233	7	US-11-128-900-15
25	991.5	79.8	233	7	US-11-128-900-67

26	985	79.2	234	7	US-11-128-900-17	Sequence 17, Appl
27	985	79.2	234	7	US-11-128-900-69	Sequence 69, Appl
28	982.5	79.0	666	6	US-10-981-356A-30	Sequence 30, Appl
29	982.5	79.0	667	7	US-11-096-046-30	Sequence 30, Appl
30	982	79.0	218	7	US-11-158-505-12	Sequence 12, Appl
31	982	79.0	218	7	US-11-158-505-20	Sequence 20, Appl
32	982	79.0	236	7	US-11-086-289-20	Sequence 20, Appl
33	978.5	78.7	235	7	US-11-086-289-16	Sequence 16, Appl
34	977	78.6	236	7	US-11-086-289-8	Sequence 8, Appl
35	970.5	78.1	239	7	US-11-177-648-10	Sequence 10, Appl
36	967.5	77.8	238	7	US-11-177-648-35	Sequence 35, Appl
37	966	77.7	236	7	US-11-144-248-48	Sequence 48, Appl
38	966	77.7	236	7	US-11-144-222-48	Sequence 48, Appl
39	966	77.7	236	7	US-11-182-343-48	Sequence 48, Appl
40	963.5	77.5	238	7	US-11-177-648-80	Sequence 80, Appl
41	962	77.4	236	7	US-11-144-248-52	Sequence 52, Appl
42	962	77.4	236	7	US-11-144-222-52	Sequence 52, Appl
43	962	77.4	236	7	US-11-182-343-52	Sequence 52, Appl
44	961	77.3	236	7	US-11-086-289-4	Sequence 4, Appl
45	960.5	77.3	238	7	US-11-177-648-36	Sequence 36, Appl

#### ALIGNMENTS

RESULT 1  
US-10-981-356A-29  
; Sequence 29, Application US/10981356A  
; Publication No. US20060015952A1  
; GENERAL INFORMATION:  
; APPLICANT: FILVAROFF, ELLEN H.  
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT  
; FILE REFERENCE: P2068R1  
; CURRENT APPLICATION NUMBER: US/10/981.356A  
; CURRENT FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: US 60/520,398  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/557,951  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 29  
; LENGTH: 666  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized  
US-10-981-356A-29

Query Match	84.0%	Score 1043.5;	DB 6;	Length 666;
Best Local Similarity	91.4%;	Pred. No. 2.6e-61;		
Matches	201;	Conservative	9;	Mismatches
				Indels 1; Gaps 1;
Qy	21	DIWMSQSPDSLAVSLGERTVLNCKSSQSLAYSGNOKNYLAWYQKQSGSKLLIYASAR	80	
Db	1	DIWMTQSPSSLAIVAGEKVTMSCKSSQSVLYSSNOKNYLAWYQKQSGSKLLIYASTR	60	
Qy	81	ESGVPRFSGSGGTDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLEKRTVAAPS	140	
Db	61	ESGVPRDFTGSGSGTDTFTLTISVQAEADVAVYCHQYVSSD-TFGGCTKLEIKRTVAAPS	119	
Qy	141	VFIPTPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYTS	200	
Db	120	VFIPTPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYTS	179	
Qy	201	LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	240	
Db	180	LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	219	

RESULT 2

US-11-096-046-29  
; Sequence 29, Application US/11096046  
; Publication No. US20050276802A1

```
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROPF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
; US-11-096-046-29

Query Match      84.0%; Score 1043.5; DB 7; Length 667;
Best Local Similarity 91.4%; Pred. No. 2.6e-61;
Matches 201; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLAWYQOKPQSPKLLIYWASAR 80
DB 1 DIWMTQSPSLAVSAGEKVTMSCKSSQSLYSSNQKNYLAWYQOKPQSPKLLIYWASTR 60

QY 81 ESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVTAA 140
DB 61 ESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVTAA 119

QY 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
DB 120 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 179

QY 201 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
DB 180 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 219

RESULT 3
US-11-158-505-1
; Sequence 1, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
; US-11-158-505-1

Query Match      83.7%; Score 1040; DB 7; Length 238;
Best Local Similarity 84.6%; Pred. No. 1.8e-61;
Matches 203; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLA 60
DB 1 METDTILLWLLWVPGSGTDIVMTQSPDSLAVSLGERATINCKASQSDYDGD--SYMN 58

QY 61 WYQOKPQSPKLLIYWASARESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSY 120
DB 59 WYQOKPQSPKLLIYWASARESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSY 118

QY 121 PLTFGAGTKLELKRVTAAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 119 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 4
US-11-158-505-3
; Sequence 3, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 3
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
; US-11-158-505-3

Query Match      83.7%; Score 1040; DB 7; Length 238;
Best Local Similarity 84.6%; Pred. No. 1.8e-61;
Matches 203; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLYSGNQKNYLA 60
DB 1 METDTILLWLLWVPGSGTDIVMTQSPDSLAVSLGERATINCKASQSDYDGD--SYMN 58

QY 61 WYQOKPQSPKLLIYWASARESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSY 120
DB 59 WYQOKPQSPKLLIYWASARESGVPRFSGSGSGTDTLTITSSVQAEADVAVYVCOQYYSY 118

QY 121 PLTFGAGTKLELKRVTAAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 180
DB 119 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 5
US-11-158-505-25
; Sequence 25, Application US/11158505
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; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
US-11-158-505-11

Query Match      82.9%; Score 1030; DB 7; Length 238;
Best Local Similarity 84.2%; Pred. No. 7.9e-61;
Matches 202; Conservative 15; Mismatches 21; Indels 2; Gaps 1;

QY 1 MDSQAQVLMMLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
DB 1 METDTILLVLLWVPGSTGDIWMTQSPDSLAVSLGERATINCKASQSDYDGD--SYMN 58

QY 61 WYQKQGPQPKLLIYWASARESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYS 120
DB 59 WYQKQGPQPKLLIYVANSLESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQSLQD 118

QY 121 PLTFGAGTKLELKRVTVAAPSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 180
DB 119 PPTFGGKTVKIRVTVAALSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 9
US-11-158-505-17
; Sequence 17, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 17
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain sequence
US-11-158-505-17

Query Match      82.9%; Score 1030; DB 7; Length 238;
Best Local Similarity 84.2%; Pred. No. 7.9e-61;
Matches 202; Conservative 15; Mismatches 21; Indels 2; Gaps 1;

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QY 1 MDSQAQVLMMLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
DB 1 METDTILLVLLWVPGSTGDIWMTQSPDSLAVSLGERATINCKASQSDYDGD--SYMN 58

QY 61 WYQKQGPQPKLLIYWASARESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYS 120
DB 59 WYQKQGPQPKLLIYVANSLESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQSLQD 118

QY 121 PLTFGAGTKLELKRVTVAAPSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 180
DB 119 PPTFGGKTVKIRVTVAALSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 10
US-11-158-505-19
; Sequence 19, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
US-11-158-505-19

Query Match      82.9%; Score 1030; DB 7; Length 238;
Best Local Similarity 84.2%; Pred. No. 7.9e-61;
Matches 202; Conservative 15; Mismatches 21; Indels 2; Gaps 1;

QY 1 MDSQAQVLMMLLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
DB 1 METDTILLVLLWVPGSTGDIWMTQSPDSLAVSLGERATINCKASQSDYDGD--SYMN 58

QY 61 WYQKQGPQPKLLIYWASARESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYS 120
DB 59 WYQKQGPQPKLLIYVANSLESGVDPFRFSGSGSGTDFTLTISSVQAEADVAVVYCCQSLQD 118

QY 121 PLTFGAGTKLELKRVTVAAPSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 180
DB 119 PPTFGGKTVKIRVTVAALSVFIFFPSDEQLKSGTASVCLLNFPYFREAKVQWKVDNAL 178

QY 181 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 11
US-11-158-505-74
; Sequence 74, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-28

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Query Match      80.5%; Score 1000.5; DB 6; Length 666;
Best Local Similarity 86.8%; Pred. No. 1.6e-58;
Matches 191; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 21 DIVMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNKNYLAWYQOKPGQSPKLLIYWASAR 80
Db 1 DIQMTQSPSLSASVGRVITITCRASQSVLYSSNKNYLAWYQOKPGKAPKLLIYWASTR 60

QY 81 ESGVPRFSGSGGTDFTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140
Db 61 ESGVPRFSGSGGTDFTLTITSSLPQEDFATYICHQYLSSD-TFGQGTKEIKRTVAAPS 119

QY 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 120 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 179

QY 201 LSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 LSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 219

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RESULT 15

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US-11-096-046-27
; Sequence 27, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-27

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Query Match      80.5%; Score 1000.5; DB 7; Length 666;
Best Local Similarity 86.8%; Pred. No. 1.6e-58;
Matches 191; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 21 DIVMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNKNYLAWYQOKPGQSPKLLIYWASAR 80
Db 1 DIQMTQSPSLSASVGRVITITCRASQSVLYSSNKNYLAWYQOKPGKAPKLLIYWASTR 60

QY 81 ESGVPRFSGSGGTDFTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELKRITVAAPS 140
Db 61 ESGVPRFSGSGGTDFTLTITSSLPQEDFATYICHQYLSSD-TFGQGTKEIKRTVAAPS 119

QY 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 120 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 179

QY 201 LSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 LSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 219

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Search completed: February 16, 2006, 10:43:39  
Job time : 9.88889 secs

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Qy      121 PL-TFGAGTKLRLKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 179
Db      116 PMCSFGOGTKLEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 175
Qy      180 LOSGNSQESVTEODSKDSTYSLSSTLTLSCADYEKHKVYACEVTHOGLSSPTKSPNRGE 239
Db      176 LOSGNSQESVTEODSKDSTYSLSSTLTLSCADYEKHKVYACEVTHOGLSSPTKSPNRGE 235
Qy      240 C 240
Db      236 C 236

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Search completed: February 16, 2006, 10:25:01  
 Job time : 26.6667 secs

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